

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 14, 2004, 18:38:23 ; Search time 18 Seconds

(without alignment)  
1220.756 Million cell updates/sec

Title: US-10-040-884-3

Perfect score: 2192

Sequence: 1 MGMTMLLECSLSKLCVIO.....LYAAVAGIRVESLFYNYSM 422

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_42:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	446.5	20.4	806	1	CEK2_CHICK
2	444	20.3	801	1	FGR3_MOUSE
3	444	20.3	806	1	FGR3_HUMAN
4	434	19.8	802	1	FGR4_HUMAN
5	433	19.8	821	1	FGR2_MOUSE
6	428.5	19.5	822	1	FGR1_MOUSE
7	427.5	19.5	808	1	FGR4_MOUSE
8	427	19.5	821	1	FGR2_HUMAN
9	424	19.3	819	1	FGR1_CHICK
10	424	19.3	822	1	FGR1_HUMAN
11	419	19.1	746	1	ABL_MVAB
12	419	19.1	1123	1	ABL_MOUSE
13	417	19.0	1130	1	ABL_HUMAN
14	416	19.0	812	1	FGR1_XENLA
15	415	18.9	822	1	FGR1_RAT
16	415	18.9	823	1	CEK3_CHICK
17	407.5	18.6	1182	1	ABL2_HUMAN
18	403.5	18.4	439	1	ABL_FSVHY
19	397	18.1	813	1	FGR2_XENLA
20	391	17.8	1138	1	TIE1_HUMAN
21	390	17.8	1134	1	TIE1_MOUSE
22	388	17.7	729	1	FGR1_DROME
23	388	17.7	1136	1	TIE1_BOVIN
24	384	17.5	1520	1	ABL_DROME
25	382	17.4	773	1	CD96_DROME
26	379	17.3	506	1	SRK4_SPOLA
27	376.5	17.2	1052	1	FGR2_DROME
28	373	17.0	370	1	SEA_AVLET
29	370.5	16.9	825	1	TRKC_PIG
30	369	16.8	992	1	FLT3_MOUSE
31	368.5	16.8	1224	1	ABL1_CAEEL
32	367.5	16.8	778	1	TRKA_CHICK
33	366	16.7	1115	1	RET_MOUSE

34	365	16.7	1097	1	PGDR_RAT
35	364	16.6	450	1	CSK_HUMAN
36	363.5	16.6	1040	1	EG15_CAEEL
37	363.5	16.6	1087	1	PGDS_XENLA
38	362.5	16.5	993	1	FLT3_HUMAN
39	362	16.5	505	1	SRK1_SPOLA
40	362	16.5	1378	1	RON_MOUSE
41	361.5	16.5	450	1	CSK_RAT
42	361	16.5	786	1	RTKL_DROME
43	360.5	16.4	1125	1	TIE2_BOVIN
44	360	16.4	1125	1	SRK2_SPOLA
45	360	16.4	1098	1	PGDR_MOUSE

## ALIGNMENTS

RESULT 1  
CEK2\_CHICK STANDARD; PRT; 806 AA.  
AC P18450;  
DT 01-NOV-1990 (Rel. 16, Created)  
DT 01-NOV-1990 (Rel. 16, Last sequence update)  
DE 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Tyrosine kinase receptor CEK2 precursor (EC 2.7.1.112).  
GN CEK2.  
OS Gallus gallus (Chicken).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
OC Gallus.  
OX NCBI\_TaxID=9031;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=90332672; PubMed=2165604;  
RA Pasquale E.B.;  
RT "A distinctive family of embryonic protein-tyrosine kinase  
receptors.";  
RL Proc. Natl. Acad. Sci. U.S.A. 87:5812-5816(1990).  
CC -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein  
tyrosine phosphate  
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.  
CC -!- SIMILARITY: Belongs to the fibroblast growth factor receptor  
family.  
CC -!- SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.  
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or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch))  
EMBL; M35195; AAA48664.1; -  
PIR; A35963; A35963.  
DR HSSP; P11362; 1FGK.  
DR InterPro; IPR007110; IG-like.  
DR InterPro; IPR003598; IG\_c2.  
DR InterPro; IPR000719; Prot\_kinase.  
DR InterPro; IPR001245; Tyr\_pkinase.  
DR InterPro; IPR008266; Tyr\_pkinase\_AS.  
DR Pfam; PF00047; IG\_3.  
DR Pfam; PF00069; pkinase\_1.  
DR PRINTS; PR00109; TYRKINASE.  
DR ProDom; PD000001; Prot\_kinase; 1.  
DR SMART; SM00408; IGC2; 3.  
DR SMART; SM00219; TyrKc; 1.  
DR PROSITE; PS00835; IG LIKE; 3.  
DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.  
DR PROSITE; PS00011; PROTEIN\_KINASE\_DOM; 1.  
DR PROSITE; PS00109; PROTEIN\_KINASE\_TYR; 1.  
KW Receptor; Glycoprotein; Tyrosine-protein kinase; ATP-binding;  
Transferase; Phosphorylation; Transmembrane; Immunoglobulin domain;





RA Superti-Furga A., Eich G., Bucher H.U., Wisser J., Giedion A.,  
 RA Gitzelmann R., Steinmann B.;  
 RT "A glycine 375-to-cysteine substitution in the transmembrane domain  
 RT of the fibroblast growth factor receptor-3 in a newborn with  
 RT achondroplasia.";  
 RL Eur. J. Pediatr. 154:215-219(1995).  
 RN [10]  
 RP VARIANT TD1 CYS-249.  
 RX MEDLINE=95291326; PubMed=8589699;  
 RA Tavormina P.L., Rimoin D.L., Cohn D.H., Zhu Y.-Z., Shiang R.,  
 RA Wasmuth J.J.;  
 RT "Another mutation that results in the substitution of an unpaired  
 RT cysteine residue in the extracellular domain of FGFR3 in  
 RT thanatophoric dysplasia type I.";  
 RL Hum. Mol. Genet. 4:2175-2177(1995).  
 RN [11]  
 RP VARIANTS TD1 CYS-248 AND CYS-371, AND VARIANT TD2 GLU-650.  
 RX MEDLINE=95291326; PubMed=7773297;  
 RA Tavormina P.L., Shiang R., Thompson L.M., Zhu Y.-Z., Wilkin D.J.,  
 RA Lachman R.S., Wilcox W.R., Rimoin D.L., Cohn D.H., Wasmuth J.J.;  
 RT "Thanatophoric dysplasia (types I and II) caused by distinct  
 RT mutations in fibroblast growth factor receptor 3.";  
 RL Nat. Genet. 9:321-328(1995).  
 RN [12]  
 RP VARIANT HYPOCHONDROPLASIA LYS-540.  
 RX MEDLINE=95400307; PubMed=7670477;  
 RA Bellus G.A., McIntosh I., Smith E.A., Avlsworth A.S., Kaitila I.,  
 RA Horton W.A., Greenhaw G.A., Hecht J.T., Francomano C.A.;  
 RT "A recurrent mutation in the tyrosine kinase domain of fibroblast  
 RT growth factor receptor 3 causes hypochondroplasia.";  
 RL Nat. Genet. 10:357-359(1995).  
 RN [13]  
 RP VARIANT CROUZON GLU-391.  
 RX MEDLINE=96083601; PubMed=7493034;  
 RA Meyers G.A., Orlow S.J., Munro I.R., Przylepa K.A., Jabs E.W.;  
 RT "Fibroblast growth factor receptor 3 (FGFR3) transmembrane mutation  
 RT in Crouzon syndrome with acanthosis nigricans.";  
 RL Nat. Genet. 11:462-464(1995).  
 RN [14]  
 RP CHARACTERIZATION OF VARIANT ACH ARG-380.  
 RX MEDLINE=96174812; PubMed=8599935;  
 RA Webster M.K., Donoghue D.J.;  
 RT "Constitutive activation of fibroblast growth factor receptor 3 by  
 RT the transmembrane domain point mutation found in achondroplasia.";  
 RL EMBO J. 15:520-527(1996).  
 RN [15]  
 RP VARIANTS TD1 CYS-248; CYS-249; CYS-370 AND CYS-373.  
 RX MEDLINE=96254981; PubMed=8845844;  
 RA Rousseau F., el Ghoulzi V., Delezoide A.L., Legeai-Mallet L.,  
 RA le Merrer M., Munnich A., Bonaventure J.;  
 RT "Missense FGFR3 mutations create cysteine residues in thanatophoric  
 RT dwarfism type I (TD1).";  
 RL Hum. Mol. Genet. 5:509-512(1996).  
 RN [16]  
 RP VARIANT CRS3 ARG-250.  
 RX MEDLINE=97195541; PubMed=9042914;  
 RA Muenke M., Gripp K.W., McDonald-McGinn D.M., Gaudenz K.,  
 RA Whitaker L.A., Bartlett S.P., Markowitz R.I., Robin N.H., Nwokoro N.,  
 RA Mulvihill J.J., Losken H.W., Mulliken J.B., Guttmacher A.E.,  
 RA Wilroy R.S., Clarke L.A., Holloway G., Aides L.C., Haan E.A.,  
 RA Mulley J.C., Cohen M.M. Jr., Bellus G.A., Francomano C.A.,  
 RA Moloney D.M., Wall S.A., Wilkie A.O.M., Zackai E.H.;  
 RT "A unique point mutation in the fibroblast growth factor receptor 3  
 RT gene (FGFR3) defines a new craniosynostosis syndrome.";  
 RL Am. J. Hum. Genet. 60:555-564(1997).  
 RN [17]  
 RP VARIANT TD1 CYS-370.  
 RX MEDLINE=99004917; PubMed=9790257;  
 RA Katsumata N., Kuno T., Miyazaki S., Mikami S., Nagashima-Miyokawa A.,  
 RA Nishimura A., Horikawa R., Tanaka T.;  
 RT "G370C mutation in the FGFR3 gene in a Japanese patient with  
 RT thanatophoric dysplasia.";  
 RL Endocr. J. 45:S171-S174(1998).

RN [18]  
 RP VARIANT HYPOCHONDROPLASIA VAL-538.  
 RA Grigelloni G., Hagenaes L., Ekloef O., Neumeyer L., Haerleid P.E.,  
 RA Anvret M.;  
 RT "A novel missense mutation Ile538Val in the fibroblast growth  
 RT factor receptor 3 in hypochondroplasia.";  
 RL Hum. Mutat. 11:333-333(1998).  
 RN [19]  
 RP VARIANT HYPOCHONDROPLASIA THR-540.  
 RX MEDLINE=98112422; PubMed=9452043;  
 RA Deutz-Terlouw P.P., Losekoot M., Aalfs C.M., Hennekam R.C.M.,  
 RA Bakker E.;  
 RT "Asn540Thr substitution in the fibroblast growth factor receptor 3  
 RT tyrosine kinase domain causing hypochondroplasia.";  
 RL Hum. Mutat. Suppl. 1:S62-S65(1998).  
 RN [20]  
 RP VARIANT TD1 MET-650.  
 RA Kitoh H., Brodie S.G., Kupke K.G., Lachman R.S., Wilcox W.R.;  
 RT "Lys650Met substitution in the tyrosine kinase domain of the  
 RT fibroblast growth factor receptor gene causes thanatophoric dysplasia  
 RT type I.";  
 RL Hum. Mutat. 12:362-363(1998).  
 RN [21]  
 RP VARIANTS BLADDER AND CERVIX CANCERS CYS-248; CYS-249; CYS-370 AND  
 RP GLU-650.  
 RX MEDLINE=99400545; PubMed=10471491;  
 RA Cappellen D., De Oliveira C., Ricol D., Gil Diez de Medina S.,  
 RA Bourdin J., Sastre-Garau X., Chopin D., Thierry J.P., Radvanyi F.;  
 RT "Frequent activating mutations of FGFR3 in human bladder and cervix  
 RT carcinomas.";  
 RL Nat. Genet. 23:18-20(1999).  
 CC -!- FUNCTION: RECEPTOR FOR ACIDIC AND BASIC FIBROBLAST GROWTH FACTORS.  
 CC -!- PREFERENTIALLY BINDS FGF1.  
 CC -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein  
 CC tyrosine phosphate.  
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -!- ALTERNATIVE PRODUCTS:  
 CC Event=Alternative splicing; Named isoforms=3;  
 CC Name=1; Synonyms=11ic;  
 CC IsoId=P22607-1; Sequence=Displayed;  
 CC Name=2; Synonyms=11ib;  
 CC IsoId=P22607-2; Sequence=VSP\_002988;  
 CC Name=3;  
 CC IsoId=P22607-3; Sequence=VSP\_002989;  
 CC -!- TISSUE SPECIFICITY: EXPRESSED IN BRAIN, KIDNEY AND TESTIS. VERY  
 CC LOW OR NO EXPRESSION IN SPLEEN, HEART, AND MUSCLE. IN 20- TO 22-  
 CC WEEK OLD FETUSES IT IS EXPRESSED AT HIGH LEVEL IN KIDNEY, LUNG,  
 CC SMALL INTESTINE AND BRAIN, AND TO A LOWER DEGREE IN SPLEEN, LIVER,  
 CC AND MUSCLE. EPITHELIAL CELLS SHOW EXCLUSIVELY ISOFORM 2  
 CC TRANSCRIPTS WHILE FIBROBLASTIC CELLS SHOW A MIXTURE OF ISOFORMS 1  
 CC AND 2 TRANSCRIPTS.  
 CC -!- DISEASE: Defects in FGFR3 are the cause of achondroplasia (ACH)  
 CC [MIM:100800]. ACH is an autosomal dominant disease and is the most  
 CC frequent form of short-limb dwarfism. It is characterized by a  
 CC long, narrow trunk, short extremities, particularly in the

Query Match 20.3%; Score 444; DB 1; Length 806;  
 Best Local Similarity 30.5%; Pred. No. 2e-26;  
 Matches 117; Conservative 74; Mismatches 161; Indels 32; Gaps 8;  
 QY 34 VTIFLILGLVTLWLFIREQRTQQQSGP---QGIAPVPPPPDLGSWAGHGNGVALPL-KE 89  
 DB 381 VGFFLFVLVAAVTLCLRPKPKGLSPVTHKLSRFLPKRQVLSNASHSSNTPLVRI 440  
 QY 90 TSVENFLGATTPALAKIQVP-----REQLSVLEQICSGSCGPIFRANNTGDP 139  
 DB 441 ARLSSGEGPTLVNVSLELPADPKWLSRLTLGKPLGEGCFGVVMAEAIQDKRAA 500  
 QY 140 KPKSVILKALKEPAGLHEVDFLGRIOFHQVLGHKNVLQEGCTEKLPLYMWLEDAQ 199  
 DB 501 KPVTAVKMLKDDATDKDLSDVSEMMKMGKHKHNIINLLGACTQGGPLYLVEYAAK 560  
 QY 200 GDLLGLWTCRRDVTMTDGLLY-----DLTEKQVHIGKQVLLALEFLOEKHLFH 249





FT DISULFID 271 333 POTENTIAL.  
 FT CARBOHYD 112 112 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 258 258 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 290 290 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 311 311 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 322 322 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT VARIANT 388 388 G -> R (in dbSNP:351855).  
 FT CONFLICT 297 297 D -> V (IN REF. 1).  
 FT SEQUENCE 802 AA; 87954 MW; B22B259831BB889F CRC64;  
 Query Match 19.8%; Score 434; DB 1; Length 802;  
 Best Local Similarity 29.8%; Pred. No. 1.2e-25;  
 Matches 119; Conservative 77; Mismatches 164; Indels 40; Gaps 12;  
 QY 21 EKOYEVLIV---PTLAVTIFLLILGLVILWLFIREQRTQOQRSGP-----QGIAPVPPRDL 73  
 Db 364 EARYTDLILVAGSLALAVLLLAGL-----YRQALHGRHPRPPATVOKLSRFFLARQF 418  
 QY 74 SNEAGHGNNVALPL-KETSVENFLGATTPALAKLQVPREQLSE-----VL-RQICSGSC 125  
 Db 419 SLESGSGKSSSLVGRVSSSGPALLAGLVSLDLPDLWFFPRDLVLGKPLGEGCF 478  
 QY 126 GPIFRAMNTGDSKP---KSVILKALKEPAGLHEVQDFLGRIOFHOYLKGNLVLQLEG 182  
 Db 479 GQVRAEAFGMDPAREDOASTVAVKMLKONASDKLADLVSEVMVKLIGRHKNIINLLG 538  
 QY 183 CTEKPLPLVWLDVDAQDGLGLFWTCRRDV---MTMDG-----LLYDLTEKQVYVHG 232  
 Db 539 VCTQEGELVIVCAKGNLREFL-RARRPPGPDLPDGRPSRSEGPLSPFVLVSCAY--- 594  
 QY 233 KOVLLALEFLQKHLFHDVGAARNILMQSDLTAKLGLGLAYEVYTRGAISSQT--IPL 290  
 Db 595 -QVARGMQLSRKCIHRDLAARNVLVTEDNVWKIADFLGARGVHHIDYKYKTSNGRLPV 653  
 QY 291 KWLAPRLLLRPASIRADVWSFGILLIYEMVTLCAPYEPVPPPTSIHLHOKRKIMRPPS 350  
 Db 654 KWMAPALPDVRYTHOSDVMWSFGILLWEITFLGSGSPYGPVPELPSLLREGRHMDRPPH 713  
 QY 351 CTHMYTSIMKSWREADRPSPRELRLRLRLAAIKTADDE 390  
 Db 714 CPPELYGLMRECHWAAPSQRPTFKQLVEALDKVLLAVSEE 753

## RESULT 5

FGR2 MOUSE  
 ID FGR2 MOUSE STANDARD; PRT; 821 AA.  
 AC P21803; 055141; Q00389; Q61342;  
 DT 01-MAY-1991 (Rel. 18, Created)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Fibroblast growth factor receptor 2 precursor (EC 2.7.1.112) (FGFR-2)  
 DE (Keratinocyte growth factor receptor).  
 GN FGFR2 OR ECT1 OR BEK.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 [1]  
 RN SEQUENCE FROM N.A. (ISOFORM LONG).  
 RP TISSUE=Brain, and Liver;  
 RX MEDLINE=92228773; PubMed=1373495;  
 RA Mansukhani A., Dell'Era P., Moscattelli D., Kornbluth S.,  
 RA Hanafusa H., Basilico C.;  
 RT "Characterization of the murine BEK fibroblast growth factor (FGF)  
 RT receptor: activation by three members of the FGF family and  
 RT requirement for heparin.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 89:3305-3309(1992).  
 [2]

RT "PCR-based identification of new receptors: molecular cloning of a  
 RT receptor for fibroblast growth factors.";  
 RL Oncogene 6:753-760(1991).  
 RN [3]  
 RP SEQUENCE FROM N.A. (ISOFORM SHORT).  
 RX MEDLINE=91095977; PubMed=1846048;  
 RA Miki T., Fleming T.P., Bottaro D.P., Rubin J.S., Ron D.,  
 RA Aaronson S.A.;  
 RT "Expression cDNA cloning of the KGF receptor by creation of a  
 RT transforming autoexon loop.";  
 RL Science 251:72-75(1991).  
 RN [4]  
 RP SEQUENCE FROM N.A. (ISOFORM LONG).  
 RX MEDLINE=98167854; PubMed=9499422;  
 RA Twigg S.R.F., Burns H.D., Oldridge M., Heath J.K., Wilkie A.O.M.;  
 RT "Conserved use of non-canonical 5' splice site (GA) in alternative  
 RT splicing by fibroblast growth factor receptors 1, 2 and 3.";  
 RL Hum. Mol. Genet. 7:685-691(1998).  
 RN [5]  
 RP SEQUENCE OF 477-821 FROM N.A.  
 RC TISSUE=Liver;  
 RX MEDLINE=89219016; PubMed=2468939;  
 RA Kornbluth S., Paulson K.E., Hanafusa H.;  
 RT "Novel tyrosine kinase identified by phosphotyrosine antibody  
 RT screening of cDNA libraries.";  
 RL Mol. Cell. Biol. 8:5541-5544(1988).  
 CC -1- FUNCTION: RECEPTOR FOR ACIDIC AND BASIC FIBROBLAST GROWTH FACTORS.  
 CC POSSESSES A HIGHER AFFINITY FOR ACIDIC THAN FOR BASIC EGF'S.  
 CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein  
 CC tyrosine phosphate.  
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -1- ALTERNATIVE PRODUCTS:  
 CC Event=Alternative splicing; Named isoforms=2;  
 CC Name=Long;  
 CC IsoId=P21803-1; Sequence=Displayed;  
 CC Name=Short;  
 CC IsoId=P21803-2; Sequence=VSP\_002985, VSP\_002986, VSP\_002987;  
 CC -1- SIMILARITY: Belongs to the fibroblast growth factor receptor  
 CC family.  
 CC -1- SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.  
 CC -----  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC EMBL; M86441; AAA37286.1; -;  
 CC EMBL; X55441; CAA39083.1; -;  
 CC EMBL; M63503; AAA39377.1; -;  
 CC EMBL; Y16152; CAA76098.1; -;  
 CC EMBL; Y16167; CAA76099.1; -;  
 CC EMBL; M23362; AAA37285.1; -;  
 CC PIR; A44142; TVMSBK.  
 CC PIR; S17295; S17295.  
 CC HSSP; P11362; 1FGK.  
 CC MGD; MGI:95523; Fgfr2.  
 CC GO; GO:0007435; P:salivary gland morphogenesis; IMP.  
 CC InterPro; IPR007110; Ig-like.  
 CC InterPro; IPR003598; Ig\_c2.  
 CC InterPro; IPR000719; Prot\_kinase.  
 CC InterPro; IPR001245; Tyr\_kinase.  
 CC InterPro; IPR008266; Tyr\_kinase\_AS.  
 CC Pfam; PF00047; ig; 3.  
 CC Pfam; PF00069; pkinase; 1.  
 CC PRINTS; PR00109; TYRKINASE.  
 CC ProDom; PD000001; Prot\_kinase; 1.  
 CC SMART; SM00408; Igc2; 3.  
 CC SMART; SM00219; Tyrc; 1.  
 CC PROSITE; PS50835; IG-LIKE; 3.  
 CC PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.

DR PROSITE; PS00011; PROTEIN KINASE DOM; 1.  
 DR PROSITE; PS00109; PROTEIN\_KINASE\_TYR; 1.  
 KW Receptor; Glycoprotein; Tyrosine-protein kinase; ATP-binding;  
 KW Transferase; Phosphorylation; Transmembrane; Signal;  
 KW Immunoglobulin domain; Repeat; Alternative splicing.  
 FT SIGNAL 1 21  
 FT CHAIN 22 821  
 FT DOMAIN 22 377  
 FT TRANSMEM 378 398  
 FT DOMAIN 399 821  
 FT DOMAIN 39 125  
 FT DOMAIN 154 247  
 FT DOMAIN 256 358  
 FT DOMAIN 481 770  
 FT NP BIND 487 495  
 FT BINDING 517 517  
 FT ACT SITE 626 626  
 FT MOD RES 657 657  
 FT DISULFID 62 107  
 FT DISULFID 179 231  
 FT DISULFID 278 342  
 FT CARBOHYD 83 83  
 FT CARBOHYD 123 123  
 FT CARBOHYD 147 147  
 FT CARBOHYD 228 228  
 FT CARBOHYD 241 241  
 FT CARBOHYD 265 265  
 FT CARBOHYD 297 297  
 FT CARBOHYD 318 318  
 FT CARBOHYD 331 331  
 FT VARSPLIC 37 37  
 FT VARSPLIC 38 152  
 FT VARSPLIC 314 361  
 FT AAGVNTDKIEVLVIRNVTEDAGEYTCLAGNSIGISGFHS  
 FT AMLTVLP -> HSGINSNAEVLALFNVTENDAGYICKVS  
 FT NYIGQASAMITVLPKQ (in isoform Short).  
 FT /FTID=VSP 002987.  
 FT A -> V (IN REF. 2).  
 FT GE -> RG (IN REF. 2).  
 FT E -> R (IN REF. 2).  
 FT E -> Y (IN REF. 2).  
 FT DV -> R (IN REF. 2).  
 FT C -> V (IN REF. 2 AND 3).  
 FT S -> P (IN REF. 2 AND 3).  
 FT W -> R (IN REF. 2).  
 FT Y -> I (IN REF. 2).  
 FT E -> R (IN REF. 2).  
 FT N -> Y (IN REF. 2).  
 FT SEQUENCE 821 AA; 91983 MW; FCDB28ADD61F4414 CRC64;  
 Query Match 19.8%; Score 433; DB 1; Length 821;  
 Best Local Similarity 27.9%; Pred. No. 1.5e-25;  
 Matches 118; Conservative 84; Mismatches 165; Indels 56; Gaps 10;  
 QY 19 IQEKQVEIVITLL-----VTIFILGLVILWLFIREQRTQQRSGQGIA----- 65  
 Db 364 VREK--EITASDYLEIAYICGVFLIACNVTVIFCRMKTTTKPDESSQAVHKLTKR 421  
 QY 66 -PVPPRDLWSAGHGNNVALPKETSVENFLGATTPALA-----KIQVPREQ 113  
 Db 422 IFLRRQVTVSAESSSSMNSNTPLVTRITRLSSATDTPMLAGVSEVELPDPKWEFPDKL 481  
 QY 114 SEVLEIQCSGCGPIFRANWNTGDSKPK---SVILKALKBPAGLHEVODFLGRQFQHY 170  
 Db 482 T-LGKPLGSGCGQVVMABAVGIDKPKPEAVTVAVVLMKDDATEKDLSDLVSEMEMMKM 540  
 QY 171 LGKHKNLVLEGCTEKLPLYMVLVDVAQDGLLGLWTCRRDVTMTDGLYD----- 222  
 Db 541 IGRHKNIINLLGACTQDGLYVIVEYASKGNREYLRARRPPGMEYS----YDINRVPEQ 597  
 QY 223 LYEKQVYHIGKQVLLALEFLQEKHLPHGVDVAARNILMQSDLTAKLGLGLA-----Y 274

Db 598 MTFKDLVSCYQLARGMEYLASQKCIHRDLAARNVLVTENNVMKIADFLGARDINNIDY 657  
 QY 275 EYVTRGAISSTQTITPLKWLAPERLLRPASIRADVWSGILLYEMVTLCAPPYEPVPPTS 334  
 Db 658 KKTNG-----RUPVKMAPEALFDVYTHQSDVWSGVLWELFTLGGSPYGPVVEE 711  
 QY 335 ILELQRRKIMKRPSSCTHTMYSIMKSCWRREADRSPRELRLLEAAIKTADDEAVLQ 394  
 Db 712 LFKLLKEGHRMDKPTNCTNCTNELYMMWRDCWHAVPSQRTFKQLVEDLRLTLTITNEBYLD 771  
 QY 395 VPE 397  
 Db 772 LTQ 774  
 RESULT 6  
 FGRI\_MOUSE  
 ID FGRI\_MOUSE STANDARD; PRT; 822 AA.  
 AC P16092; Q01736; Q61562;  
 DT 01-APR-1990 (Rel. 14, Created)  
 DT 01-MAY-1991 (Rel. 18, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Basic fibroblast growth factor receptor 1 precursor (EC 2.7.1.112)  
 GN FGFR1 (bFGF-R) (MFR).  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10990;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Brain;  
 RX MEDLINE=90160373; PubMed=1689490;  
 RA Reid H.H., Wilks A.F., Bernard O.;  
 RT "Two forms of the basic fibroblast growth factor receptor-like mRNA  
 are expressed in the developing mouse brain.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 87:1596-1600(1990).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BALB/c; TISSUE=Brain;  
 RX MEDLINE=90265603; PubMed=2161096;  
 RA Safran A., Avioli A., Orr-Urtreger A., Neufeld G., Lonai P.,  
 RA Givol D., Yarden Y.;  
 RT "The murine flg gene encodes a receptor for fibroblast growth  
 factor.";  
 RL Oncogene 5:635-643(1990).  
 RN [3]  
 RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.  
 RX MEDLINE=91207411; PubMed=1708247;  
 RA Kouhara H., Kasayama S., Saito H., Matsumoto K., Sato B.;  
 RT "Expression cDNA cloning of fibroblast growth factor (FGF) receptor  
 in mouse breast cancer cells: a variant form in FGF-responsive  
 transformed cells.";  
 RL Biochem. Biophys. Res. Commun. 176:31-37(1991).  
 RN [4]  
 RP SEQUENCE FROM N.A. (ISOFORM 2).  
 RX MEDLINE=90272715; PubMed=2161540;  
 RA Mansukhani A., Moscattelli D., Talarico D., Levyska V., Basilico C.;  
 RT "A murine fibroblast growth factor (FGF) receptor expressed in CHO  
 cells is activated by basic FGF and Kaposi FGF.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 87:4378-4382(1990).  
 RN [5]  
 RP SEQUENCE OF 1-15 FROM N.A., AND ALTERNATIVE SPLICING.  
 RX MEDLINE=95100926; PubMed=7802632;  
 RA Harada T., Saito H., Kouhara H., Kurebayashi S., Kasayama S.,  
 RA Terakawa N., Kishimoto T., Sato B.;  
 RT "Murine fibroblast growth factor receptor 1 gene generates multiple  
 messenger RNAs containing two open reading frames via alternative  
 splicing.";  
 RL Biochem. Biophys. Res. Commun. 205:1057-1063(1994).  
 CC -!- FUNCTION: Receptor for basic fibroblast growth factor. A shorter  
 form of the receptor could be a receptor for acidic FGF (aFGF).  
 CC -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein

tyrosine phosphate.

-!- SUBCELLULAR LOCATION: Type I membrane protein.

-!- ALTERNATIVE PRODUCTS:

Event=Alternative splicing; Named isoforms=3;

Name=1;

IsoId=P16092-1; Sequence=Displayed;

Name=2;

IsoId=P16092-2; Sequence=VSP\_002962;

Name=3; Synonyms=Variant;

IsoId=P16092-3; Sequence=VSP\_002961, VSP\_002963;

-!- SIMILARITY: Belongs to the fibroblast growth factor receptor family.

-!- SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.

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EMBL; M28998; AAA37290.1; -

EMBL; X51893; CAA36175.1; -

EMBL; M65053; AAA37620.1; -

EMBL; M33760; AAA37622.1; -

EMBL; S74765; AAB32845.1; ALT\_SEQ.

PIR; A34849; TVMSFG.

HSSP; P11362; 1FGK.

MGI; 98522; Fgfr1.

GO; GO:0007420; P:brain development; IMP.

GO; GO:0042472; P:inner ear morphogenesis; IMP.

GO; GO:0007435; P:salivary gland morphogenesis; IMP.

InterPro; IPR007110; Ig-like.

InterPro; IPR003598; Ig\_c2.

InterPro; IPR00719; Prot\_kinase.

InterPro; IPR001245; Tyr\_kinase.

InterPro; IPR008266; Tyr\_kinase\_AS.

Pfam; PF00047; Ig; 3.

Pfam; PF00069; pkinase; 1.

PRINTS; P00109; TYRKINASE.

ProDom; PD000001; Prot\_kinase; 1.

SMART; SM00408; IGC2; 3.

SMART; SM00219; TyrK; 1.

PROSITE; PS00835; IG\_LIKE; 3.

PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.

PROSITE; PS00011; PROTEIN\_KINASE\_DOM; 1.

PROSITE; PS00109; PROTEIN\_KINASE\_TYR; 1.

Receptor; Glycoprotein; Tyrosine-protein kinase; ATP-binding; Transferase; Phosphorylation; Transmembrane; Signal; Immunoglobulin domain; Repeat; Alternative splicing.

SIGNAL 1 21

POTENTIAL.

CHAIN 22 822

BASIC FIBROBLAST GROWTH FACTOR RECEPTOR

1.

DOMAIN 22 376

EXTRACELLULAR (POTENTIAL).

TRANSMEM 377 397

POTENTIAL.

DOMAIN 398 822

CYTOPLASMIC (POTENTIAL).

DOMAIN 25 119

IG-TOPIK C2-TYPE 1.

DOMAIN 158 246

IG-LIKE C2-TYPE 2.

DOMAIN 255 357

IG-LIKE C2-TYPE 3.

DOMAIN 478 767

PROTEIN KINASE.

NP\_BIND 484 492

ATP (BY SIMILARITY).

BINDING 514 514

ATP (BY SIMILARITY).

ACT\_SITE 623 623

BY SIMILARITY.

MOD\_RES 654 654

PHOSPHORYLATION (AUTO-) (BY SIMILARITY).

DISULFID 55 101

POTENTIAL.

DISULFID 178 230

POTENTIAL.

DISULFID 277 341

POTENTIAL.

CARBOHYD 77 77

N-LINKED (GLCNAC. . .) (POTENTIAL).

CARBOHYD 117 117

N-LINKED (GLCNAC. . .) (POTENTIAL).

CARBOHYD 227 227

N-LINKED (GLCNAC. . .) (POTENTIAL).

CARBOHYD 240 240

N-LINKED (GLCNAC. . .) (POTENTIAL).

CARBOHYD 264 264

N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 296 296 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 317 317 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 330 330 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT VARSPLIC 30 30 Q -> QGSSSWPLWAAA (in isoform 3).

FT VARSPLIC 31 119 Missing (in isoform 2).

FT VARSPLIC 148 149 Missing (in isoform 3).

FT VARSPLIC 149 149 Missing (in isoform 3).

FT CONFLICT 229 229 T -> S (IN REF. 4).

FT CONFLICT 256 258 ILQ -> HPS (IN REF. 1 AND 3).

FT CONFLICT 270 270 G -> A (IN REF. 4).

FT CONFLICT 387 387 I -> M (IN REF. 3).

FT CONFLICT 440 440 G -> A (IN REF. 2).

FT CONFLICT 508 508 V -> L (IN REF. 3).

FT CONFLICT 544 544 I -> M (IN REF. 4).

FT CONFLICT 756 756 R -> H (IN REF. 1).

FT CONFLICT 765 765 E -> D (IN REF. 4).

SQ SEQUENCE 822 AA; 91980 MW; D5A4695FAG80926B CRC64;

Query Match 19.5%; Score 428.5; DB 1; Length 822;

Best Local Similarity 27.1%; Pred. No. 3.3e-25;

Matches 114; Conservative 87; Mismatches 182; Indels 37; Gaps 8;

QY 11 SLSDKLCVIOEKQY-EVIIVPTLLVIFLLILGLVILWLF---IREQTOOQSGGPOGIAP 66

Db 361 ALBERPAVMTSPYLEIIIIYCTGAFILSCMLGVIIYKMSGTTKSDFSQMAVHLAKS 420

QY 67 VPPPRDLSEAGHGNNVALPKETSVENFLGATTPALA-----KLQVPEQ--L 113

Db 421 IPLRQVTVSADSSASMSNGVLLVPSRLSSSGTPEMLAGVSEYELPEDPRWELPRDLVL 480

QY 114 SEVLQICSGSCGPIFRANMTGDSKPKSVILKALKEPAGLHEVODFLGRQPHYLQK 173

Db 481 GKPLGEGCGQVLAIEGLDKDKNRVTKVAVKMLKSDATKDLSDLSIEMEMMKMGK 540

QY 174 HKNLVQEGCCTEKLPLYMVLDEVAQDILLGLFWTCRRDVTMDGLY-----DL 223

Db 541 HKNIIILGACTQDGLVIVIVYVASKGNLREYLQARR-----PPGLECYNFSHNPBEQL 595

QY 224 TEKQVYHGKQVLLALEFLQEKHLFHGDVAARNILMQSDLTAKLGLGLAYEYVYTRGATS 283

Db 596 SSKDLVSCAYQVARGMEVLAASKKTHRDLAARNVLVTEDEVNWKIADFLGARDTHIDYVK 655

QY 284 STQT--IPLKWLAPERLLLRPASIRADVMSFGILLVEMVTLGAPVPEVPTSIHLQOR 341

Db 656 KTTNGRLPVKNWAPALFDRIYTHQSDVMSFGVLLWEIFTLGSGPYGPGVVEELFKLKE 715

QY 342 RKIMKRPSSCTHTMYSIMKSCWRREADRPSRELRLRLAEAIKTADDEAVLQVPELVVP 401

Db 716 GHRMDKPSNCTNELYMMRDCWHAVPSQRPPTFKQLVEDLDRIVALTNSQEYL---DLSTP 772

RESULT 7

FCR4 MOUSE

ID FCR4 MOUSE STANDARD; PRT; 808 AA.

AC Q03142;

DT 01-OCT-1994 (Rel. 30, Created)

DT 01-OCT-1996 (Rel. 34, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Fibroblast growth factor receptor 4 precursor (EC 2.7.1.112) (FGFR-4)

DE (Protein-tyrosine kinase receptor MPK-11).

GN FGFR4 OR FGFR-4 OR MPK-11.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI\_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=CD-1; TISSUE=Fetal cerebellum;

RX MEDLINE=92146274; PubMed=1723680;

RA Stark K.L.; McMahon J.; McMahon A.P.;

RT "FGFR-4, a new member of the fibroblast growth factor receptor



RT genome.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 87:8180-8184(1990).  
 RN [3]  
 RP SEQUENCE FROM N.A. (ISOFORM 17).  
 RX MEDLINE=91274356; PubMed=1647213;  
 RA Seno M., Sasada R., Watanabe T., Ishimaru K., Igarashi K.;  
 RT "Two cDNAs encoding novel human FGF receptor.";  
 RL Biochim. Biophys. Acta 1089:244-246(1991).  
 RN [4]  
 RP SEQUENCE FROM N.A. (ISOFORM 4).  
 RC TISSUE=Stomach cancer;  
 RX MEDLINE=90332706; PubMed=2377625;  
 RA Hattori Y., Odagiri H., Nakatani H., Miyagawa K., Naito K.,  
 RT Sakamoto H., Katoh O., Yoshida T., Sugimura T., Terada M.;  
 RA "K-sam, an amplified gene in stomach cancer, is a member of the  
 RT heparin-binding growth factor receptor genes.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 87:5983-5987(1990).  
 RN [5]  
 RP SEQUENCE FROM N.A. (ISOFORMS 5; 14 AND 15).  
 RX MEDLINE=92212948; PubMed=1313574;  
 RA Katoh M., Hattori Y., Sasaki H., Tanaka M., Sugano K., Yazaki Y.,  
 RT Sugimura T., Terada M.;  
 RA "K-sam gene encodes secreted as well as transmembrane receptor  
 RT tyrosine kinase.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 89:2960-2964(1992).  
 RN [6]  
 RP SEQUENCE FROM N.A. (ISOFORM 3).  
 RC TISSUE=Placenta;  
 RX MEDLINE=93016048; PubMed=1400433;  
 RA Dell K.R., Williams L.T.;  
 RT "A novel form of fibroblast growth factor receptor 2. Alternative  
 RT splicing of the third immunoglobulin-like domain confers ligand  
 RT binding specificity.";  
 RL J. Biol. Chem. 267:21225-21229(1992).  
 RN [7]  
 RP SEQUENCE FROM N.A. (ISOFORMS 3 AND 19), AND VARIANT ARG-613.  
 RC TISSUE=Mammary gland;  
 RX MEDLINE=92108030; PubMed=1309608;  
 RA Miki T., Bottaro D.P., Fleming T.P., Smith C.L., Burgess W.H.,  
 RT Chan A.M.-L., Aaronson S.A.;  
 RT "Determination of ligand-binding specificity by alternative splicing:  
 RT two distinct growth factor receptors encoded by a single gene.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 89:246-250(1992).  
 RN [8]  
 RP SEQUENCE FROM N.A. (ISOFORM 19).  
 RC TISSUE=Breast, and Cornea;  
 RX MEDLINE=95170769; PubMed=7866434;  
 RA Wilson S.E., Weng J., Chwang E.L., Gollahon L., Leitch A.M.,  
 RT Shay J.W.;  
 RT "Hepatocyte growth factor (HGF), keratinocyte growth factor (KGF), and  
 RT their receptors in human breast cells and tissues: alternative  
 RT receptors.";  
 RL Cell. Mol. Biol. Res. 40:337-350(1994).  
 RN [9]  
 RP ERRATUM.  
 RC TISSUE=Breast, and Cornea;  
 RA Wilson S.E., Weng J., Chwang E.L., Gollahon L., Leitch A.M.,  
 RT Shay J.W.;  
 RL Cell. Mol. Biol. Res. 40:707-707(1994).  
 RN [10]  
 RP SEQUENCE FROM N.A. (ISOFORM 1), AND VARIANT CS SER-342.  
 RC TISSUE=Blood;  
 RA Steinberger D., Mueller U.;  
 RL Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.  
 RN [11]  
 RP SEQUENCE FROM N.A. (ISOFORMS 7; 9; 10; 11; 12 AND 13), AND VARIANT  
 RP ARG-613.  
 RX MEDLINE=20090220; PubMed=10626794;  
 RA Ueda T., Sasaki H., Kuwahara Y., Nezu M., Shibuya T., Sakamoto H.,  
 RA Ishii H., Yanagihara K., Maifune K.-I., Makuuchi M., Terada M.;  
 RT "Deletion of the carboxyl-terminal exons of K-sam/FGFR2 by short  
 RT homology-mediated recombination, generating preferential expression  
 RT of specific messenger RNAs.";  
 RL Nat. Genet. 8:98-103(1994).  
 RN [12]  
 RP SEQUENCE FROM N.A. (ISOFORMS 5; 6; 8; 14 AND 18).  
 RX MEDLINE=21845873; PubMed=11856867;  
 RA Ingersoll R.G., Paznekas W.A., Tran A.K., Scott A.F., Jiang G.,  
 RT Jabs E.W.;  
 RT "Fibroblast growth factor receptor 2 (FGFR2): genomic sequence and  
 RT variations.";  
 RL Cytogenet. Cell Genet. 94:121-126(2001).  
 RN [13]  
 RP SEQUENCE FROM N.A. (ISOFORM 3).  
 RA Lind D.L., Cox D.R.;  
 RT "Sequence and polymorphisms in fibroblast growth factor receptor 2  
 RT (FGFR2) gene in humans.";  
 RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.  
 RN [14]  
 RP SEQUENCE OF 314-427 FROM N.A.  
 RX MEDLINE=20177482; PubMed=10712195;  
 RA Glaser R.L., Jiang W., Boyadjiev S.A., Tran A.K., Zachary A.A.,  
 RT Van Maldergem L., Johnson D., Walsh S., Oldridge M., Wall S.A.,  
 RA Wilkie A.O.M., Jabs E.W.;  
 RT "Paternal origin of FGFR2 mutations in sporadic cases of Crouzon  
 RT syndrome and Pfeiffer syndrome.";  
 RL Am. J. Hum. Genet. 66:768-777(2000).  
 RN [15]  
 RP SEQUENCE OF 1-209; 212-767 AND 771-821 FROM N.A. (ISOFORMS 5; 14 AND  
 RP 18).  
 RX MEDLINE=99214070; PubMed=10196476;  
 RA Zhang Y., Gorri M.C., Post J.C., Ehrlich G.D.;  
 RT "Genomic organization of the human fibroblast growth factor receptor 2  
 RT (FGFR2) gene and comparative analysis of the human FGFR gene family.";  
 RL Gene 230:69-79(1999).  
 RN [16]  
 RP SEQUENCE OF 249-313 FROM N.A. AND VARIANTS AS TRP-252 AND ARG-253.  
 RX MEDLINE=93397814; PubMed=7668257;  
 RA Park W.-J., Theda C., Maestri N.E., Meyers G.A., Fryburg J.S.,  
 RT Dufresne C., Cohen M.M. Jr., Jabs E.W.;  
 RT "Analysis of phenotypic features and FGFR2 mutations in Apert  
 RT syndrome.";  
 RL Am. J. Hum. Genet. 57:321-328(1995).  
 RN [17]  
 RP SEQUENCE OF 251-259 FROM N.A.  
 RX MEDLINE=96253074; PubMed=8676562;  
 RA Wada C., Ishigaki M., Toyooka Y., Yamabe H., Ohnuki Y., Takada F.,  
 RT Yamazaki Y., Ohtani H.;  
 RT "Nucleotide sequences at intron 6 and exon 7 junction of fibroblast  
 RT growth factor receptor 2 and rapid mutational analysis in Apert  
 RT syndrome.";  
 RL Rinsho Byori 44:435-438(1996).  
 RN [18]  
 RP SEQUENCE OF 251-318 FROM N.A.  
 RX MEDLINE=96241572; PubMed=8673103;  
 RA Moloney D.M., Slaney S.F., Oldridge M., Wall S.A., Sahlin P.,  
 RA Stenman G., Wilkie A.O.M.;  
 RT "Exclusive paternal origin of new mutations in Apert syndrome.";  
 RL Nat. Genet. 13:48-53(1996).  
 RN [19]  
 RP SEQUENCE OF 263-361 FROM N.A. AND VARIANTS CS PRO-289; ARG-338;  
 RP SER-342; TYR-342; GLY-344 AND CYS-354.  
 RX MEDLINE=96090259; PubMed=7581378;  
 RA Gorri M.C., Preston R.A., White G.J., Zhang Y., Singhal V.K.,  
 RT Losken H.W., Parker M.G., Nwokoro N.A., Post J.C., Ehrlich G.D.;  
 RT "Crouzon syndrome: mutations in two spliceforms of FGFR2 and a common  
 RT point mutation shared with Jackson-Weiss syndrome.";  
 RL Hum. Mol. Genet. 4:1387-1390(1995).  
 RN [20]  
 RP VARIANTS CS HIS-340; ARG-342; TYR-342 AND CYS-354.  
 RX MEDLINE=95078932; PubMed=7987400;  
 RA Reardon W., Winter R.M., Rutland P., Pulleyn L.J., Jones B.M.,  
 RA Malcolm S.;  
 RT "Mutations in the fibroblast growth factor receptor 2 gene cause  
 RT Crouzon syndrome.";  
 RL Nat. Genet. 8:98-103(1994).



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[21]
RN RP VARIANTS CS CYS-328 AND CYS-347, AND VARIANT JWS GLY-344.
RX MEDLINE=95179174; PubMed=7874170;
RA Jabs E.W., Li X., Scott A.F., Meyers G.A., Chen W., Eccles M., Mao J.,
RN Charnas L.R., Jackson C.E., Jabs E.W.,
RT "Jackson-Weiss and Crouzon syndromes are allelic with mutations in
RL fibroblast growth factor receptor 2.";
RN Nat. Genet. 8:275-279(1994).
[22]
RN RP VARIANTS CS.
RX MEDLINE=95384152; PubMed=7655462;
RA Oldridge M., Wilkie A.O.M., Staney S.F., Poole M.D., Pulleyn L.J.,
RN Rutland P., Hockley A.D., Wake M.J.C., Goldin J.H., Winter R.M.,
RA Reardon W., Malcolm S.;
RT "Mutations in the third immunoglobulin domain of the fibroblast growth
RL factor receptor-2 gene in Crouzon syndrome.";
RN Hum. Mol. Genet. 4:1077-1082(1995).
[23]
RN RP VARIANTS CS GLY-290; TRP-342 AND CYS-354, AND VARIANT JWS ARG-342.
RX MEDLINE=96133301; PubMed=8528214;
RA Park W.-J., Meyers G.A., Li X., Theda C., Day D., Orlow S.J.,
RN Jones M.C., Jabs E.W.;
RT "Novel FGFR2 mutations in Crouzon and Jackson-Weiss syndromes show
RL Query Match 19.5%; Score 427; DB 1; Length 821;
Best Local Similarity 27.4%; Pred. No. 4.2e-25;
Matches 115; Conservative 84; Mismatches 167; Indels 54; Gaps 9;
QY 22 KQYEVIPTLL-----VTFLILLGVLMFLFREQTQOORSQOIA-----PV 67
Db 365 REKEITASPDYLEIAIYIGVFLIACMVVTIVLCMKNTTKKPDFSQPAVHKLTKRIPL 424
QY 68 PPRDLNSWAGHGNNALPLKETSVENFLGATTPALA-----KLVPRQELSEV 116
Db 425 RQVTVSASSSSSNSNTPLVRIITRLSSDTATPMLAGVSEVELPEDPKWEPFRDKLT-L 483
QY 117 LEQICSGSCGPIFRANMNTGPSKPK---SVILKALKEPAGIHEVQDFLGRIQHQLGK 173
Db 484 GKPLGEGCFGVMAEAGVGDKPKKAVTVAVXMKDKDATEKDLVSEWEMKMGK 543
QY 174 HKNLVQEGCCTEKLPLMVLVEDVAQDGLLGLFWTCRRDVTMDGLLYD-----LTE 225
Db 544 HKNINLLGACTQDGPLYVIVEYASKGNLREYLRRRPPGMEYS---YDINRVPEQMTF 600
QY 226 KOVYHIGQVLLALEFLOEKHLFHGDVAARNLQSDLTAKLCGLGLA-----YEVY 277
Db 601 KDLVSCVQLARGMEYLAQKCIHRDLAARNVLTENNVMKIADPGLARDINNIDYKKT 660
QY 278 TRGAISSTQITPLKWLAPERLLLRPASIRADVMSFGILLYEMVTILGAPPYEPVPTSL 337
Db 661 TNG-----RLPVKMAPEALFDRVYTHQSDVMSFGVLMWEIFTLGSGSPYGPVVEELFK 714
QY 338 HLQRRKIMKRSSCTHTMYSTKSCWRWRADRPSPRELRLRLAIAKYTADDEAVLQVPE 397
Db 715 LLKRGHRMDKPNACTNLYMMRDCWHAVPSPQRTFKQLVEDLDRILTLTTNEEYLDLSQ 774
RESULT 9
FGRL_CHICK
ID FGRL_CHICK STANDARD; PRT; 819 AA.
AC P21804;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Basic fibroblast growth factor receptor 1 precursor (BC 2.7.1.112).
GN CEK1.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
```

```
RX MEDLINE=89315814; PubMed=2473471;
RA Pasquale E.B., Singer S.J.;
RT "Identification of a developmentally regulated protein-tyrosine
RT kinase by using anti-phosphotyrosine antibodies to screen a cDNA
RL expression library.";
RN Proc. Natl. Acad. Sci. U.S.A. 86:5449-5453(1989).
[2]
RN RP REVISIONS.
RA Pasquale E.B.;
RL Submitted (MAY-1989) to the EMBL/GenBank/DBJ databases.
[3]
RN RP SEQUENCE FROM N.A.
RX MEDLINE=89298406; PubMed=2544996;
RA Lee P.L., Johnson D.E., Cousens L.S., Fried V.A., Williams L.T.;
RT "Purification and complementary DNA cloning of a receptor for basic
RT fibroblast growth factor.";
RL Science 245:57-60(1989).
CC -!- FUNCTION: RECEPTOR FOR BASIC FIBROBLAST GROWTH FACTOR.
CC -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
CC tyrosine phosphate.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: Belongs to the fibroblast growth factor receptor
CC family.
CC -!- SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.
-----
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RX EMBL; M24637; AAA48663.1; -.
DR PIR; A41345; TVCHFQ.
DR HSSP; P11362; 1FGK.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003598; IG_c2.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR001245; Tyr_kinase.
DR InterPro; IPR008266; Tyr_kinase_AS.
DR Pfam; PF00047; Ig; 3.
DR Pfam; PF00069; pkinase; 1.
DR PRINTS; PR00109; TYRKINASE.
DR PRODOM; PD000001; Prot_kinase; 1.
DR SMART; SM00408; Igc2; 3.
DR SMART; SM00219; TyrK; 1.
DR PROSITE; PS50835; IG LIKE; 3.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS50011; PROTEIN KINASE DOM; 1.
DR PROSITE; PS00109; PROTEIN KINASE_TYR; 1.
KW Receptor; Glycoprotein, Tyrosine-protein kinase; ATP-binding;
KW Transferase; Phosphorylation; Transmembrane; Immunoglobulin domain;
KW Repeat; Signal.
FT SIGNAL 1 21
FT CHAIN 22 819
FT DOMAIN 22 374
FT TRANSMEM 375 395
FT DOMAIN 396 819
FT DOMAIN 33 118
FT DOMAIN 145 244
FT DOMAIN 253 355
FT DOMAIN 125 132
FT DOMAIN 476 765
FT NP_BIND 482 490
FT BINDING 512 512
FT ACT_SITE 621 621
FT MOD_RES 652 652
FT DISULFID 54 100
FT DISULFID 176 228
FT DISULFID 275 339
FT CARBOHYD 76 76
FT POTENTIAL.
FT BASIC FIBROBLAST GROWTH FACTOR RECEPTOR
FT 1.
FT EXTRACELLULAR (POTENTIAL).
FT POTENTIAL.
FT CYTOPLASMIC (POTENTIAL).
FT IG-LIKE C2-TYPE 1.
FT IG-LIKE C2-TYPE 2.
FT IG-LIKE C2-TYPE 3.
FT ASP/GLU-RICH (HIGHLY ACIDIC).
FT PROTEIN KINASE.
FT ATP (BY SIMILARITY).
FT ATP (BY SIMILARITY).
FT BY SIMILARITY.
FT PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT POTENTIAL.
FT POTENTIAL.
FT N-LINKED (GLCNAC...) (POTENTIAL).
```



EMBO J. 9:2685-2692(1990).  
[3]  
RN SEQUENCE FROM N.A.  
RN MEDLINE=92282615; PubMed=1317750;  
RX Hattori Y., Odagiri H., Katch O., Sakamoto H., Morita T.,  
RA Shimotohno K., Tobinai K., Sugimura T., Terada M.;  
RA "K-sam-related gene, N-sam, encodes fibroblast growth factor receptor  
RT and is expressed in T-lymphocytic tumors.";   
RN Cancer Res. 52:3367-3371(1992).  
RN [4]  
RN SEQUENCE FROM N.A.  
RN TISSUE=Liver;  
RX MEDLINE=91126480; PubMed=1846977;  
RX Hou J., Kan M., McKeehan K., McBride G., Adams P., McKeehan W.L.;  
RA "Fibroblast growth factor receptors from liver vary in three  
RT structural domains.";   
RN science 251:665-668(1991).  
RN [5]  
RN SEQUENCE FROM N.A.  
RX MEDLINE=92118399; PubMed=1662973;  
RX Kiefer M.C., Baird A., George-Nascimento C., Nguyen T., Mason O.B.,  
RA Boley L.J., Valenzuela P., Barr P.J.;  
RA "Molecular cloning of a human basic fibroblast growth factor receptor  
RT cDNA and expression of a biologically active extracellular domain in  
RT a baculovirus system";   
RN Growth Factors 5:115-127(1991).  
RN [6]  
RN SEQUENCE FROM N.A.  
RX TISSUE=Placenta;  
RX MEDLINE=90290512; PubMed=2162671;  
RX Itoh N., Terachi T., Ohka M., Seo M.K.;  
RA "The complete amino acid sequence of the shorter form of human basic  
RT fibroblast growth factor receptor deduced from its cDNA.";   
RN Biochem. Biophys. Res. Commun. 169:680-685(1990).  
RN [7]  
RN SEQUENCE OF 201-822 FROM N.A.  
RA Ruta M., Hawk R., Ricca G., Drohan W., Zabelshansky M., Laureys G.,  
RA Barton D.E., Francke U., Schlessinger J., Givol D.;  
RA "A novel protein tyrosine kinase gene whose expression is modulated  
RT during endothelial cell differentiation.";   
RN Oncogene 3:9-15(1988).  
RN [8]  
RN SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.  
RX MEDLINE=90355989; PubMed=2167437;  
RX Johnson D.E., Lee P.L., Lu J., Williams L.T.;  
RT "Diverse forms of a receptor for acidic and basic fibroblast growth  
RT factors";   
RN Mol. Cell. Biol. 10:4728-4736(1990).  
RN [9]  
RN ALTERNATIVE SPLICING.  
RX MEDLINE=91141499; PubMed=1847500;  
RX Gutkind S.J., Link D.C., Katamine S., Lacal P., Miki T., Ley T.J.,  
RA Robbins K.C.;  
RT "A novel c-fgr exon utilized in Epstein-Barr virus-infected B  
RT lymphocytes but not in normal monocytes.";   
RN Mol. Cell. Biol. 11:1500-1507(1991).  
RN [10]  
RN SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.  
RX TISSUE=Lung;  
RX MEDLINE=91319400; PubMed=1650441;  
RX Eisenmann A., Ahn J.A., Graziani G., Tronick S.R., Ron D.;  
RA "Alternative splicing generates at least five different isoforms of  
RT the human basic-FGF receptor.";   
RN Oncogene 6:1195-1202(1991).  
RN [11]  
RN SEQUENCE FROM N.A.  
RX Wennstroem S., Sandstroem C., Claesson-Welsh L.;  
RA Submitted (JUL-1990) to the EMBL/GenBank/DBAJ databases.  
RN [12]  
RN SEQUENCE FROM N.A. (ISOFORM ALPHA B1).  
RX TISSUE=Uterus;  
RX MEDLINE=22388257; PubMed=12477932;  
RX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RESULT 10	FCRI HUMAN	STANDARD;	PRT;	822 AA.
ID	FCRI HUMAN			
AC	P11362; P17049;			
DT	01-JUL-1989 (Rel. 11, Created)			
DT	01-MAY-1991 (Rel. 18, Last sequence update)			
DE	15-MAR-2004 (Rel. 43, Last annotation update)			
DE	Basic fibroblast growth factor receptor 1 precursor (EC 2.7.1.112)			
DE	(FGFR-1) (bFGF-R) (Fms-like tyrosine kinase-2) (c-fgr).			
GN	FGFR1 OR FLG OR FGPER OR FLT2.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
OX	{1}_TaxID=9606;			
RP	SEQUENCE FROM N.A.			
RP	TISSUE=Placenta;			
RX	MEDLINE=90245600; PubMed=2159626;			
RA	Isacchi A., Bergonzoni L., Sarmientos P.;			
RA	"Complete sequence of a human receptor for acidic and basic			
RT	fibroblast growth factors.";			
RT	Nucleic Acids Res. 18:1906-1906 (1990).			
RN	[2]			
RN	SEQUENCE FROM N.A.			
RP	TISSUE=Neonatal brain stem;			
RP	MEDLINE=90360977; PubMed=1697263;			
RA	Dionne C.A., Crumley G.R., Bellot F., Kaplow J.M., Searfoss G.,			
RA	Ruta M., Burgess W.H., Jaye M., Schlessinger J.;			
RA	"Cloning and expression of two distinct high-affinity receptors			
RT	cross-reacting with acidic and basic fibroblast growth factors.";			
RT				



RT structural similarity of its transforming gene product to other onc  
RT gene products with tyrosine-specific kinase activity.";  
RL Proc. Natl. Acad. Sci. U.S.A. 80:3623-3627(1983).  
RN [2]  
RA REDDYS TO 588-746.  
RA Reddy E.P., Smith M.J., Srinivasan A.;  
RL Proc. Natl. Acad. Sci. U.S.A. 80:7372-7372(1983).  
RN [3]  
RP SEQUENCE OF 233-327 FROM N.A.  
RX MEDLINE=83245023; PubMed=6191223;  
RA Groffen J., Heisterkamp N., Reynolds F.H. Jr., Stephenson J.R.;  
RT "Homology between phosphotyrosine acceptor site of human c-abl and  
RT viral oncogene products";  
RL Nature 304:167-169(1983).  
CC -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein  
CC tyrosine phosphate.  
CC -!- MISCELLANEOUS: THIS PROTEIN IS SYNTHESIZED AS A GAG-ABL  
CC POLYPEPTIDE.  
CC -!- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. ABL  
CC SUBFAMILY.  
CC -!- SIMILARITY: Contains 1 SH2 domain.  
CC  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC  
CC EMBL; V01541; -; NOT ANNOTATED\_CDS.  
DR EMBL; K00010; AAA46470.1; -;  
DR HSP; P00519; 2ABL.  
DR InterPro; IPR000719; Prot\_kinase.  
DR InterPro; IPR000980; SH2.  
DR InterPro; IPR001245; Tyr\_kinase.  
DR InterPro; IPR008266; Tyr\_pkinase\_AS.  
DR Pfam; PF00069; pkinase; 1.  
DR Pfam; PF00017; SH2; 1.  
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DR PRINTS; PR00109; TYRKINASE.  
DR ProDom; PD000001; Prot\_kinase; 1.  
DR ProDom; PD000093; SH2; 1.  
DR SMART; SM00252; SH2; 1.  
DR SMART; SM00219; TyrKc; 1.  
DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.  
DR PROSITE; PS00109; PROTEIN\_KINASE\_TYR; 1.  
DR PROSITE; PS50011; PROTEIN\_KINASE\_DOM; 1.  
DR PROSITE; PS50001; SH2; 1.  
KW Polyprotein; Transferase; Tyrosine-protein kinase; ATP-binding;  
KW Oncogene; SH2 domain.  
FT DOMAIN 13 103 SH2  
FT DOMAIN 128 379 PROTEIN\_KINASE.  
FT NP\_BIND 134 142 ATP (BY SIMILARITY).  
FT BINDING 157 157 ATP (BY SIMILARITY).  
FT ACT\_SITE 249 249 BY SIMILARITY.  
SQ SEQUENCE 746 AA; 81872 MW; B9072FFP55PE9257 CRC64;  
  
Query Match 19.1%; Score 419; DB 1; Length 746;  
Best Local Similarity 34.7%; Pred. No. 1.5e-24;  
Matches 96; Conservative 51; Mismatches 94; Indels 36; Gaps 7;  
  
QY 143 SVTLKALKEPAGLHEVDLGRIFQHQYGLKKNLVQLEGCCPEKPLYNVLVEDVAQGD 202  
DB 153 TVAVTKLEDT--MEVEEFLKEAAVMKEI-KHENLVQLGVCTREPFFYIITEFTYGNL 209  
QY 203 LGEFLWTCRRDVTMDGLDYLTEKQVYVHIGKQVLLALEFLQEKHLPHGDAVAARNILMQSD 262  
DB 210 LDVIRECNRQEVSAVLLYMAT-----QISSAMEYLEKCNFTHRLAARNCLVGEN 260  
QY 263 LFAKLCGLGLAY-----EVYTRGAISSQTQTPKWLAPERLLLRPASIRADVWSFGILLYE 318  
DB 261 HLVKVADFGLSRLMTGDTYTAHAGAK---FPFKWTAPESLAYNKFISKSDVWAFGLLWE 317

QY 319 MYTLGAPPYVPPTTSILHQLRRKIMKRPSCCTHTMYSIMKSCWREARDPSPRELRL 378  
DB 318 IATYGMSPYGDLSQVIELLEDRMERPECPKPYELMRACWQWNTSDRPSFAEIHQ 377  
QY 379 RLEAAIK--TADDE-----AVLQVPEL 398  
DB 378 AFETMFQESSISDEVEKEIGKRGTRGGAGSMLOAPEL 414  
  
RESULT 12  
ABL1 MOUSE  
ID ABL1 MOUSE STANDARD; PRT; 1123 AA.  
AC P00520; P97896; Q61252; Q61253; Q61254; Q61255; Q61256; Q61257;  
AC Q61258; Q61259; Q61260; Q61261;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 01-JAN-1990 (Rel. 13, Last sequence update)  
DT 15-JAN-2004 (Rel. 43, Last annotation update)  
DE Proto-oncogene tyrosine-protein kinase ABL1 (EC 2.7.1.112) (p150)  
DE (c-ABL).  
GN ABL1 OR ABL.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Testis;  
RX MEDLINE=88068561; PubMed=3317402;  
RA Oppi C., Shore S.K., Reddy E.P.;  
RT "Nucleotide sequence of testis-derived c-abl cDNAs: implications for  
RT testis-specific transcription and abl oncogene activation";  
RL Proc. Natl. Acad. Sci. U.S.A. 84:8200-8204(1987).  
RN [2]  
RP SEQUENCE OF 1-187 FROM N.A. (ISOFORMS I; II; III AND IV).  
RX MEDLINE=95394474; PubMed=7665185;  
RA Chisoe S.L., Bodenteich A., Wang Y.-F., Wang Y.-P., Burian D.,  
RA Clifton S.W., Crabtree J., Freeman A., Iyer K., Jian L., Ma Y.,  
RA McLaury H.-J., Pan H.-Q., Sarhan O.H., Toth S., Wang Z., Zhang G.,  
RA Heisterkamp N., Groffen J., Roe B.A.;  
RT "Sequence and analysis of the human ABL gene, the BCR gene, and  
RT regions involved in the Philadelphia chromosomal translocation.";  
RL Genomics 27:67-82(1995).  
RN [3]  
RP SEQUENCE OF 85-182 FROM N.A.  
RX MEDLINE=84106840; PubMed=6319018;  
RA Wang J.Y.J., Ledley F., Goff S., Lee R., Groner Y., Baltimore D.;  
RT "The mouse c-abl locus: molecular cloning and characterization.";  
RL Cell 36:349-356(1984).  
RN [4]  
RP ALTERNATIVE SPLICING.  
RX MEDLINE=88202920; PubMed=3283651;  
RA Bernards A., Faskind M., Baltimore D.;  
RT "Four murine c-abl mRNAs arise by usage of two transcriptional  
RT promoters and alternative splicing.";  
RL Oncogene 2:297-304(1988).  
RN [5]  
RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF 61-121.  
RX MEDLINE=95393198; PubMed=7664083;  
RA Musacchio A., Saraste M., Wilmanns M.;  
RT "High-resolution crystal structures of tyrosine kinase SH3 domains  
RT complexed with proline-rich peptides.";  
RL Nat. Struct. Biol. 1:546-551(1994).  
RN [6]  
RP X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF 229-515.  
RX MEDLINE=20446271; PubMed=1098075;  
RA Schindler T., Bornmann W., Pellicena P., Miller W.T., Clarkson B.,  
RA Kuriyan J.;  
RT "Structural mechanism for Src-571 inhibition of abelson tyrosine  
RT kinase";  
RL Science 289:1938-1942(2000).  
CC -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein  
CC tyrosine phosphate.



OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Fibroblast;  
RX MEDLINE=90082420; PubMed=2687768;  
RA Fairstein E., Einat M., Gokkel E., Marcelle C., Croce C.M.,  
RA Gale R.P., Canaani E.;  
RT "Nucleotide sequence analysis of human abl and bcr-abl cDNAs.";  
RL Oncogene 4:1477-1481(1989).  
RN [2]  
RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.  
RX MEDLINE=87028219; PubMed=3021337;  
RA Shivelman E., Lifshitz B., Gale R.P., Roe B.A., Canaani E.;  
RT "Alternative splicing of RNAs transcribed from the human abl gene and  
from the bcr-abl fused gene.";  
RL Cell 47:277-284(1986).  
RN [3]  
RP SEQUENCE FROM N.A. (ISOFORMS IA AND IB).  
RC TISSUE=lung carcinoma;  
RX MEDLINE=95394474; PubMed=7665185;  
RA Chisoe S.L., Bodenteich A., Wang Y.-F., Wang Y.-P., Burian D.,  
RA Clifton S.W., Crabtree J., Freeman A., Iyer K., Jian L., Ma Y.,  
RA McLaury H.-J., Pan H.-Q., Sarhan O.H., Toth S., Wang Z., Zhang G.,  
RA Heisterkamp N., Groffen J., Roe B.A.;  
RT "Sequence and analysis of the human ABL gene, the BCR gene, and  
RT regions involved in the Philadelphia chromosome translocation.";  
RL Genomics 27:67-82(1995).  
RN [4]  
RP SEQUENCE OF 360-426 FROM N.A.  
RX MEDLINE=83245023; PubMed=6191223;  
RA Groffen J., Heisterkamp N., Reynolds F.H. Jr., Stephenson J.R.;  
RT "Homology between phosphotyrosine acceptor site of human c-abl and  
RT viral oncogene products.";  
RL Nature 304:167-169(1983).  
RN [5]  
RP SEQUENCE OF 27-40 FROM N.A.  
RX MEDLINE=88065859; PubMed=2825022;  
RA Fairstein E., Marcelle C., Rosner A., Canaani E., Gale R.P.,  
RA Drazan O., Smith S.D., Croce C.M.;  
RT "A new fused transcript in Philadelphia chromosome positive acute  
RT lymphocytic leukaemia.";  
RL Nature 330:386-388(1987).  
RN [6]  
RP SEQUENCE OF 825-845 FROM N.A.  
RX MEDLINE=94142331; PubMed=7545908;  
RA Inokuchi K., Futaki M., Dan K., Nomura T.;  
RT "Sequence analysis of the mutation at codon 834 and the sequence  
RT variation of codon 837 of c-abl gene.";  
RL Leukemia 8:343-344(1994).  
RN [7]  
RP STRUCTURE BY NMR OF SH2 DOMAIN.  
RX MEDLINE=92370689; PubMed=1505033;  
RA Overduin M., Rios C.B., Mayer B.J., Baltimore D., Cowburn D.;  
RT "Three-dimensional solution structure of the src homology 2 domain of  
RT c-abl.";  
RL Cell 70:697-704(1992).  
RN [8]  
RP STRUCTURE BY NMR OF SH2 DOMAIN.  
RX MEDLINE=93101588; PubMed=1281542;  
RA Overduin M., Mayer B.J., Rios C.B., Baltimore D., Cowburn D.;  
RT "Secondary structure of Src homology 2 domain of c-Abl by  
RT heteronuclear NMR spectroscopy in solution.";  
RL Proc. Natl. Acad. Sci. U.S.A. 89:11673-11677(1992).  
RN [9]  
RP STRUCTURE BY NMR OF SH3 DOMAIN.  
RX MEDLINE=96131878; PubMed=8590002;  
RA Gosser Y.Q., Zheng J., Overduin M., Mayer B.J., Cowburn D.;  
RT "The solution structure of Abl SH3, and its relationship to SH2 in  
RT the SH(32) construct";  
RL Structure 3:1075-1086(1995).  
RN [10]  
RP 3D-STRUCTURE MODELING OF SH3 DOMAIN.  
RX MEDLINE=95192229; PubMed=7892170;  
RA Pisabarro M.T., Ortiz A.R., Serrano L., Wade R.C.;  
RT "Homology modeling of the Abl-SH3 domain.";  
RL Proteins 20:203-215(1994).  
RN [11]  
RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF 57-218.  
RX MEDLINE=96398698; PubMed=88055596;  
RA Nam H.-J., Haer W.G., Roberts T.M., Frederick C.A.;  
RT "Intramolecular interactions of the regulatory domains of the Bcr-Abl  
RT kinase reveal a novel control mechanism.";  
RL Structure 4:1105-1114(1996).  
RN [12]  
RP X-RAY CRYSTALLOGRAPHY (1.65 ANGSTROMS) OF 64-121.  
RX MEDLINE=98365516; PubMed=9698566;  
RA Pisabarro M.T., Serrano L., Wilmanns M.;  
RT "Crystal structure of the Abl-SH3 domain complexed with a designed  
RT high-affinity peptide ligand: implications for SH3-ligand  
RT interactions.";  
RL J. Mol. Biol. 281:513-521(1998).  
RN [13]  
RP STRUCTURE BY NMR OF 62-122 IN COMPLEX WITH CRK.  
RX MEDLINE=22294994; PubMed=12384576;  
RA Donaldson L.W., Gish G., Pawson T., Kay L.E., Forman-Kay J.D.;  
RT "Structure of a regulatory complex involving the Abl SH3 domain, the  
RT Crk SH2 domain, and a Crk-derived phosphopeptide.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:14053-14058(2002).  
CC -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein  
CC tyrosine phosphate.  
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.  
CC -!- ALTERNATIVE PRODUCTS:  
CC Event=Alternative splicing; Named isoforms=2;  
CC Name=IA;  
CC IsoId=P00519-1; Sequence=Displayed;  
CC Name=IB;  
CC IsoId=P00519-2; Sequence=VSP 004957;  
CC -!- TISSUE SPECIFICITY: Widely expressed.  
CC -!- DISEASE: Participates in a t(9;22)(q34;q11) chromosomal  
CC translocation that produces a BCR-ABL oncogene responsible for  
CC chronic myeloid leukemia (CM), acute myeloid leukemia (AML) and  
CC acute lymphoblastic leukemia (ALL).  
CC -!- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. ABL  
CC SUBFAMILY.  
CC -!- SIMILARITY: Contains 1 SH2 domain.  
CC -!- SIMILARITY: Contains 1 SH3 domain.  
CC -!- DATABASE: NAME=Atlas Genet. Cytogenet. Oncol. Haematol.;  
CC WWW="http://www.infobiogen.fr/services/Chromancer/Genes/ABL.html".  
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DR EMBL: X16416; CAA34438.1; -  
DR EMBL: M14752; AAA51561.1; -  
DR EMBL: U07563; AAB60394.1; -  
DR EMBL: U07563; AAB60393.1; -  
DR EMBL: U07561; AAB60393.1; JOINED.  
DR EMBL: S69223; AAD14034.1; -  
DR PIR: S08519; TVHUA.  
DR PDB: 1AB2; 31-JAN-94.  
DR PDB: 2ABL; 04-SEP-97.  
DR PDB: 1AWO; 28-JAN-98.  
DR PDB: 1BBZ; 25-NOV-98.  
DR PDB: 1ABL; 01-NOV-94.  
DR PDB: 1JU5; 06-NOV-02.  
DR Genew; HGNC:76; ABL1.  
DR MIM; 169980; -  
DR GO; GO:0004713; F:protein-tyrosine kinase activity; TAS.



FT CARBOHYD 177 177 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 223 223 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 236 236 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 260 260 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 292 292 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 313 313 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 326 326 N-LINKED (GLCNAC. . .) (POTENTIAL).  
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 Matches 97; Conservative 67; Mismatches 137; Indels 26; Gaps 5;  
 QY 92 VENFLGATTPALAKL-----QVPEQ--LSEVLEQICSGSGCPIFRANMTGDP 138  
 DB 440 VRLSSSGTFLMSGLSEYELPEDPNEVARDRLILCKPLGEGCGVGVMAEALGDKERP 499  
 QY 139 SKPKSVILKALKEPAGLHEVQDFLGRIOFHYGLGKHNLVQEGCTEKLPLYMVLDDVA 198  
 DB 500 NKVTKVAVKMLKSDASEKDLSDISEMMMKMGKHNIINLLGACTQDGLYVIVEYTS 559  
 QY 199 QDILLGFLWT-----CRDVTMTDGLLYDLTEKQVHIGKQVLLALEELQEKHLPHG 250  
 DB 560 KGNLEYLRRARPPAMEYCNTPCPDQL---LSFKDLVSCAYQVARGMDYLASKCIHR 616  
 QY 251 DVAARNILMQSDILAKLGLGLGLAYEVYTRGAISSTQT--IPLKWLAPERLLLRPASIRAD 308  
 DB 617 DLAAENVLTEDNIMKIADFLGLARDIHDYKKTNGRLPVKMAPEALFDRIYTHQSD 676  
 QY 309 VMSFGILLVEMTVLGAAPPVPEPPTSILEHLQRRKTMKPPSSCTHTMYIMSKSWRREA 368  
 DB 677 VMSFGILLWEITFGSPYGVMEELFKLKEGHRMDKPTNCTNELYMMKDCWHAMPS 736  
 QY 369 DRPSPELRLEAAKTAADDAVLQV 395  
 DB 737 QRPTFNQVLVEDLRIILAUSSNOEYDDL 763

## RESULT 15

FGP1\_RAT  
 ID FGR1\_RAT STANDARD; PRT; 822 AA.  
 AC Q04589;  
 DT 01-JUN-1994 (Rel. 29, Created)  
 DT 01-JUN-1994 (Rel. 29, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Basic fibroblast growth factor receptor 1 precursor (EC 2.7.1.112)  
 DE (FGFR-1) (bFGF-R) (MFR).  
 GN FGFR1 OR FLG.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=93176824; PubMed=8382532;  
 RA Yazaki N., Hiroko F., Mitsuhiro O., Toshisuke K., Nobuyuki I.;  
 RT "The structure and expression of the FGF receptor-1 mRNA isoforms in rat tissues."  
 RL Biochim. Biophys. Acta 1172:37-42(1993).  
 CC -!- FUNCTION: Receptor for basic fibroblast growth factor. A shorter form of the receptor could be a receptor for acidic FGF (aFGF).  
 CC -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein tyrosine phosphate.  
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -!- SIMILARITY: Belongs to the fibroblast growth factor receptor family.  
 CC -!- SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial

CC entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).

CC EMEL; D12498; BAA02059.1; -  
 CC HSP; P11362; IFGK.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003598; Ig c2.  
 DR InterPro; IPR001245; Tyr\_kinase.  
 DR InterPro; IPR008266; Tyr\_kinase\_AS.  
 DR Pfam; PF00047; Ig; 3.  
 DR Pfam; PF00069; pkinase; 1.  
 DR PRINTS; PR0109; TYRKINASE.  
 DR ProDom; PD000001; Prot Kinase; 1.  
 DR SMART; SM00408; Igc2; 3.  
 DR SMART; SM00219; TyrKc; 1.  
 DR PROSITE; PS00835; IG-LIKE; 3.  
 DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.  
 DR PROSITE; PS00011; PROTEIN\_KINASE\_DOM; 1.  
 DR PROSITE; PS00109; PROTEIN\_KINASE\_TYR; 1.  
 KW Receptor; Glycoprotein; Tyrosine-protein kinase; ATP-binding;  
 KW Transferase; Phosphorylation; Transmembrane; Signal;  
 KW Immunoglobulin domain; Repeat.  
 FT SIGNAL 1 21  
 FT CHAIN 22 822  
 FT DOMAIN 22 376  
 FT TRANSMEM 377 397  
 FT DOMAIN 398 822  
 FT DOMAIN 25 119  
 FT DOMAIN 158 246  
 FT DOMAIN 255 357  
 FT DOMAIN 478 767  
 FT NP\_BIND 484 492  
 FT BINDING 514 514  
 FT ACT\_SITE 623 623  
 FT MOD\_RES 654 654  
 FT DISULFID 55 101  
 FT DISULFID 178 230  
 FT DISULFID 277 341  
 FT CARBOHYD 77 77  
 FT CARBOHYD 117 117  
 FT CARBOHYD 227 227  
 FT CARBOHYD 240 240  
 FT CARBOHYD 264 264  
 FT CARBOHYD 296 296  
 FT CARBOHYD 317 317  
 FT CARBOHYD 330 330  
 SQ SEQUENCE 822 AA; 91824 MW; E59D924D0A1DE5C5 CRC64;  
 Query Match 18.9%; Score 415; DB 1; Length 822;  
 Best Local Similarity 29.9%; Pred. No. 3.6e-24;  
 Matches 96; Conservative 67; Mismatches 128; Indels 30; Gaps 5;  
 QY 100 TPALA-----KLQVPEQ--LSEVLEQICSGSGCPIFRANMTGDPSPKSVIL 146  
 DB 454 TEMPLAGSVSELPEDPNEVARDRLILCKPLGEGCGVGVMAEALGDKKPNRTKVAV 513  
 QY 147 KALKPEAGLHEVQDFLGRIOFHYGLGKHNLVQEGCTEKLPLYMVLDDVAQDILGEL 206  
 DB 514 KMLKSDATEKDLSDISEMMMKMGKHNIINLLGACTQDGLYVIVEYTSKGNUREYL 573  
 QY 207 WTCRRDVTMTDGLLY-----DLTEKQVHIGKQVLLALEELQEKHLPHGVAARN 256  
 DB 574 QARR-----PPGLEVCYNFHNPEQLSSKDLVSCAYQVARGMEYLASKKIHRLAARN 628  
 QY 257 ILMQSDILAKLGLGLAYEVYTRGAISSTQT--IPLKWLAPERLLLRPASIRADVWSFGI 314  
 DB 629 LIVTEDNVMKIADFLGLARDIHDYKKTNGRLPVKMAPEALFDRIYTHQSDVWSFGV 688  
 QY 315 LIVEMTVLGAAPPVPEPPTSILEHLQRRKTMKPPSSCTHTMYIMSKSWRREADSPSR 374

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Db 689 LLWEFTLGGSENPVGVVEELFKLLKEGHRMDKPSNCTNELYMMMRDCWNAVPSQRPTEK 748

QY 375 ELRLRLAAIKTADDEAVLQV 395

Db 749 QLVEDLDRIVALTSNQEYLDL 769

Search completed: June 14, 2004, 18:44:46  
Job time : 19 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 14, 2004, 18:42:14 ; Search time 20 Seconds  
(without alignments)  
2029.641 Million cell updates/sec

Title: US-10-040-884-3  
Perfect score: 2192  
Sequence: 1 MGMTMLLECSLSDKLCVIQ.....LYAAVAGIRVESLFNYMSML 422

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_78: \*  
1: pir1: \*  
2: pir2: \*  
3: pir3: \*  
4: pir4: \*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	2192	100.0	422	2 T48680	hypothetical prote
2	465.5	21.2	829	2 JC4583	fibroblast growth
3	459.5	21.0	818	2 JC4058	fibroblast growth
4	455.5	20.8	822	2 S19947	fibroblast growth
5	455.5	20.8	822	2 B49151	fibroblast growth
6	453.5	20.7	800	1 TVHU2F	fibroblast growth
7	453.5	20.7	800	2 A48991	heparin-binding gr
8	447	20.4	797	2 S38579	fibroblast growth
9	446.5	20.4	806	2 A35963	protein-tyrosine k
10	444	20.3	801	2 I53363	fibroblast growth
11	444	20.3	806	1 TVHUF3	fibroblast growth
12	439.5	20.1	713	2 I50128	fibroblast growth
13	434	19.8	802	1 TVHUF4	fibroblast growth
14	433	19.8	705	2 S51635	fibroblast growth
15	433	19.8	707	2 A38429	keratinocyte growt
16	433	19.8	820	2 S17295	fibroblast growth
17	433	19.8	821	1 TVMSBK	fibroblast growth
18	432	19.7	682	2 A35969	heparin-binding gr
19	432	19.7	733	2 I43293	fibroblast growth
20	432	19.7	822	2 I45289	fibroblast growth
21	431	19.7	799	2 S18209	fibroblast growth
22	430	19.6	707	2 A54846	fibroblast growth
23	430	19.6	729	2 A56795	fibroblast growth
24	430	19.6	822	2 B54846	fibroblast growth
25	427.5	19.5	822	1 TVMSFG	fibroblast growth
26	427	19.5	821	1 TVHUF2	fibroblast growth
27	427	19.5	822	2 A45081	fibroblast growth
28	426	19.4	822	2 A41794	keratinocyte growt
29	424.5	19.4	832	2 JH0193	fibroblast growth

30	424	19.3	819	1 TVCHFG	fibroblast growth
31	424	19.3	822	1 TVHUEG	fibroblast growth
32	423	19.3	769	2 S16236	fibroblast growth
33	423	19.3	814	1 A39752	fibroblast growth
34	421	19.2	650	1 JC1450	gag-abl polyprotei
35	419	19.1	981	1 FOMVGM	kinase-related tra
36	419	19.1	1123	2 A39962	fibroblast growth
37	418	19.1	824	2 S36439	heparin-binding fi
38	417	19.0	415	2 I65223	protein-tyrosine k
39	417	19.0	1130	1 TVHUA	fibroblast growth
40	416	19.0	812	1 A36477	fibroblast growth
41	415	18.9	748	2 S41050	fibroblast growth
42	415	18.9	750	2 S41051	fibroblast growth
43	415	18.9	822	2 S29840	fibroblast growth
44	415	18.9	823	2 B35963	protein-tyrosine k
45	412	18.8	824	2 S24108	protein-tyrosine k

ALIGNMENTS

RESULT 1

T48680  
Hypothetical protein DKFZp761P1010.1 - human  
C:Species: Homo sapiens (man)  
C:Date: 05-May-2000 #sequence\_revision 05-May-2000 #text\_change 05-May-2000  
C:Accession: T48680  
R:Blum, H.; Bauersachs, S.; Mewes, H.W.; Weil, B.; Wiemann, S.  
submitted to the Protein Sequence Database, April 2000  
A:Reference number: Z24533  
A:Accession: T48680  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-422 <AAA>  
A:Cross-references: EMBL:ALJ53940  
A:Experimental source: adult amygdala; clone DKFZp761P1010  
C:Genetics:  
A>Note: DKFZp761P1010.1

Query Match	100.0%;	Score	2192;	DB	2;	Length	422;
Best Local Similarity	100.0%;	Pred. No.	6.2e-103;				
Matches	422;	Conservative	0;	Mismatches	0;	Indels	0;
Gaps	0;						
Qy	1	MGMTMLLECSLSDKLCVIQEQYEVIIPTLLVTIFILLGVILWLFIREFORTQQQSG	60				
Db	1	MGMTMLLECSLSDKLCVIQEQYEVIIPTLLVTIFILLGVILWLFIREFORTQQQSG	60				
Qy	61	PQGIAPVPPRDLSEAGHGGNVALPLKETSVENFLGATTPALAKLQVPREQLSEVLBQI	120				
Db	61	PQGIAPVPPRDLSEAGHGGNVALPLKETSVENFLGATTPALAKLQVPREQLSEVLBQI	120				
Qy	121	CSGSGCPIFRANMTGDPSPKSVILKALKEPAGHEVODFLGRIOFHQYLGHKNLVQL	180				
Db	121	CSGSGCPIFRANMTGDPSPKSVILKALKEPAGHEVODFLGRIOFHQYLGHKNLVQL	180				
Qy	181	EGCCTEKLPLYMWLEDAQDGLLGLFWTCRDDVMTDGLLYDLTEKQVYHIGKVLLALE	240				
Db	181	EGCCTEKLPLYMWLEDAQDGLLGLFWTCRDDVMTDGLLYDLTEKQVYHIGKVLLALE	240				
Qy	241	FLQEKHLPHGDAARNIIMQSDLTAKLCGLGLAYEVYTRGAISSTQTTPLKWLAPERLLL	300				
Db	241	FLQEKHLPHGDAARNIIMQSDLTAKLCGLGLAYEVYTRGAISSTQTTPLKWLAPERLLL	300				
Qy	301	RPASTRADVWFGILLYEMVTILGAPPYEPVPTSTLEHLQRRKIMKRPSSTHTMYSIMK	360				
Db	301	RPASTRADVWFGILLYEMVTILGAPPYEPVPTSTLEHLQRRKIMKRPSSTHTMYSIMK	360				
Qy	361	SCWRREADRSPRELRLRLAAIKTADDEAVLQVPELVVPELYAAVAGIRVESLFYNS	420				
Db	361	SCWRREADRSPRELRLRLAAIKTADDEAVLQVPELVVPELYAAVAGIRVESLFYNS	420				
Qy	421	ML 422					

D6 421 ML 422

## RESULT. T 2

fibroblast growth factor receptor 4B precursor - African clawed frog  
 C;Species: Xenopus laevis (African clawed frog)  
 C;Date: 10-Apr-1996 #sequence\_revision 24-May-1996 #text\_change 16-Jul-1999  
 C;Accession: JC4583  
 R;Riou, J.P.; Clavilier, L.; Boucaut, J.C.  
 Biochem. Biophys. Res. Commun. 218, 198-204, 1996  
 A;Title: Early regionalized expression of a novel Xenopus fibroblast growth factor receptor  
 A;Reference number: JC4583; PMID:96136300; PMID:8573131  
 A;Accession: JC4583  
 A;Molecule type: mRNA  
 A;Residues: 1-829 <RIO>  
 A;Cross-references: EMBL:X89807  
 A;Experimental source: embryo  
 C;Comment: This receptor is a tyrosine kinase transmembrane protein and plays an important role in the regulation of cell growth.  
 C;Superfamily: basic fibroblast growth factor receptor 1; immunoglobulin homology; proteoglycan core 1  
 C;Keywords: ATP; embryo; fibroblast; growth factor; receptor; transmembrane protein  
 F;1-26/Domain: signal sequence #status predicted <SIG>  
 F;27-829/Product: fibroblast growth factor receptor 4B #status predicted <MAT>  
 F;60-117/Domain: immunoglobulin homology <IM1>  
 F;136-148/Region: acidic  
 F;187-251/Domain: immunoglobulin homology <IM2>  
 F;287-362/Domain: immunoglobulin homology <IM3>  
 F;393-413/Domain: transmembrane #status predicted <TMW>  
 F;488-773/Domain: protein kinase homology <KIN>  
 F;496-504/Region: protein kinase ATP-binding motif

DECEMBER 2

fibroblast growth factor receptor-4 precursor - African clawed frog  
JC4058  
C:Species: *Xenopus laevis* (African clawed frog)  
C:Date: 29-Jun-1995 #sequence\_revision 14-Jul-1995 #text\_change 20-Jun-2000  
C:Accession: JC4058  
R;Shiozaki, C.; Tashiro, K.; Asano-Miyoshi, M.; Saigo, K.; Emori, Y.; Shiokawa, K.  
Gene 152, 215-219, 1995  
A:Title: Cloning of cDNA and genomic DNA encoding fibroblast growth factor receptor-4

A;Reference number: JC4058; MUID:95137391; PMID:7835703

A: Accession: JC4058

A:Molecule type: mRNA

A:Residues: 1-818 <SHT>

A;RESIDUES: I-616 (SHI)  
A:Cross-references: DDBJ:D31761: NTD:a809527: PTD:BAA06539 1: PTD:a809528

A; Cross-fel  
C: Genetics.

C:Genetics: 43/1; 125/1; 158/1; 213/1; 254/1; 318/1; 364/1; 429/1; 478/1; 556/1  
C:Superfamily: basic fibroblast growth factor receptor 1; immunoglobulin homology domain 1  
C:Keywords: ATP; growth factor receptor; transmembrane protein

F/1-26/Domain: signal sequence #status predicted <SIG>  
F/27-88/Domain: fibroblast growth factor receptor-4 #status predicted <MAT>  
F/56-110/Domain: immunoglobulin homology <IM1>  
F/132-137/Domain: acidic #status predicted <ADI>  
F/177-238/Domain: immunoglobulin homology <IM2>  
F/276-347/Domain: immunoglobulin homology <IM3>  
F/362-402/Domain: transmembrane #status predicted <TM>  
F/477-762/Domain: protein kinase homology <KIN>  
F/485-493/Region: protein kinase ATP-binding motif

DEC 11 1964

fibroblast growth factor receptor - Iberian ribbed newt  
 C/Species: Pleurodeles waltlii (Iberian ribbed newt)  
 C/Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 16-Jul-1999  
 C/Accession: S19947  
 R/Shi, D.L.; Feige, J.J.; Riou, J.F.; Desimone, D.W.; BoucAUT, J.C.  
 submitted to the EMBL Data Library, March 1992  
 A/Description: Receptors during early development of the urodele *Pleurodeles waltlii*.  
 A/Description number: S19947

Gene 132, 213-217, 1993  
A;Title: Cloning of cDNA and genomic DNA encoding fibroblast growth factor receptor-4

Query Match 20.8%; Score 455.5; DB 2; Length 822;  
Best Local Similarity 29.2%; Pred. No. 6.3e-16;  
Matches 118; Conservative 82; Mismatches 169; Indels 35; Gaps 11;

QY 21 EKQYEVIIVPT--LLVTFILLLGVILWLFIREORTQOORSGPQGIAPVPPPRDLWSWAG 78  
DB 383 ETRYTDIIIIYTSGLALLMAAVIVLCRMQLPPTKTHLEPATVHKLSRFPLMRQFSLESS 442

QY 79 HGGNVALPKETSIVENFAGATTPAL-----AKLQVPREOLSEVL--EQICSGSGC 126  
DB 443 SSGKSTSL--VRVTRLSSCTPMLPGVLEFDLPDLSKWEFFRRL--VLGKPLGEGCFG 498

QY 127 PIFRA---NMNTGDPKPKSVILKALKEPAGLHEVQDFLGRIOFHYLGKHKNLVQLGEC 183  
DB 499 QVRAEAYGINKQDPDKAITVAIKIVKDKGTDELSDLISEMELMKMGKHKNIINLLGV 558

QY 184 CTEKPLPLYMWLEDAVQAQDGLLGLFWTCRRDVTMTDGLLYDLTE-----KQVYHIGKQV 235  
DB 559 CTQDGLPLYMIVEYASKGNLREFL--RARRP--PSPDYTFDMTKVPEQLSFQDLVSCSYQV 615

QY 236 LLALFLEQKHLFGCDVAARNILMQSDLTAKLGGGLAYEVYTRGAISSTQT--IPLKWL 293  
DB 616 ARGWAYLESKRCIHRDLAARNVLTGENVMKIADPGLARGVHDIDYKKTSNGLRPLVKWM 675

QY 294 APERILLRPAIRADVMSFGILLYEMVTLGAPPYVEVPPTSILEHLQRRKIMKRPSSCTH 353  
DB 676 APEALFDRVYTHQSDVMSFGVLTWEIFTLGGSPYGPVPEELFKLLRGHRMDKPSNCTH 735

QY 354 TMSYIMSKCWREADRPSPRELRLRLEAAIKTADDEAV--LQVP 396  
DB 736 ELYMLMRECWAHAPSQRPTFKQLVETLDRILATVAEEYLDLSMP 779

RESULT 5  
B49151  
fibroblast growth factor receptor 4 - Iberian ribbed newt  
C:Species: Pleurodeles waltlii (Iberian ribbed newt)  
C:Date: 19-Dec-1993 #sequence\_revision 18-Nov-1994 #text\_change 16-Jul-1999  
C:Accession: B49151  
R:Shi, D.L.; Feige, J.J.; Riou, J.F.; DeSimone, D.W.; Boucaut, J.C.  
Development 116, 261-273, 1992  
A:Title: Differential expression and regulation of two distinct fibroblast growth factor  
A:Reference number: B49151; MUID:93130775; PMID:1483392  
A:Accession: B49151  
A>Status: preliminary  
A:Molecule type: nucleic acid  
A:Residues: 1-822 <SHI>  
A:Cross-references: GB:X65059; NID:G64252; PIDN:CAA46192.1; PID:G64253  
A:Experimental source: tail-bud  
A:Note: sequence extracted from NCBI backbone (NCBIN:122598, NCBIp:122599)  
C:Superfamily: basic fibroblast growth factor receptor 1; immunoglobulin homology; prote  
C:Keywords: ATP; growth factor receptor  
F:283-354/Domain: immunoglobulin homology <IMM>  
F:484-769/Domain: protein kinase homology <KIN>  
F:492-500/Region: protein kinase ATP-binding motif

Query Match 20.8%; Score 455.5; DB 2; Length 822;  
Best Local Similarity 29.2%; Pred. No. 6.3e-16;  
Matches 118; Conservative 82; Mismatches 169; Indels 35; Gaps 11;

QY 21 EKQYEVIIVPT--LLVTFILLLGVILWLFIREORTQOORSGPQGIAPVPPPRDLWSWAG 78  
DB 383 ETRYTDIIIIYTSGLALLMAAVIVLCRMQLPPTKTHLEPATVHKLSRFPLMRQFSLESS 442

QY 79 HGGNVALPKETSIVENFAGATTPAL-----AKLQVPREOLSEVL--EQICSGSGC 126  
DB 443 SSGKSTSL--VRVTRLSSCTPMLPGVLEFDLPDLSKWEFFRRL--VLGKPLGEGCFG 498

QY 127 PIFRA---NMNTGDPKPKSVILKALKEPAGLHEVQDFLGRIOFHYLGKHKNLVQLGEC 183  
DB 499 QVRAEAYGINKQDPDKAITVAIKIVKDKGTDELSDLISEMELMKMGKHKNIINLLGV 558

QY 184 CTEKPLPLYMWLEDAVQAQDGLLGLFWTCRRDVTMTDGLLYDLTE-----KQVYHIGKQV 235

DB 559 CTQDGLPLYMIVEYASKGNLREFL--RARRP--PSPDYTFDMTKVPEQLSFQDLVSCSYQV 615  
QY 236 LLALFLEQKHLFGCDVAARNILMQSDLTAKLGGGLAYEVYTRGAISSTQT--IPLKWL 293  
DB 616 ARGWAYLESKRCIHRDLAARNVLTGENVMKIADPGLARGVHDIDYKKTSNGLRPLVKWM 675

QY 294 APERILLRPAIRADVMSFGILLYEMVTLGAPPYVEVPPTSILEHLQRRKIMKRPSSCTH 353  
DB 676 APEALFDRVYTHQSDVMSFGVLTWEIFTLGGSPYGPVPEELFKLLRGHRMDKPSNCTH 735

QY 354 TMSYIMSKCWREADRPSPRELRLRLEAAIKTADDEAV--LQVP 396  
DB 736 ELYMLMRECWAHAPSQRPTFKQLVETLDRILATVAEEYLDLSMP 779

RESULT 6  
TVHU2P  
fibroblast growth factor receptor flg-2 precursor - human  
C:Species: Homo sapiens (man)  
C:Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 16-Jun-2000  
C:Accession: A60350; S21843  
R:Avivi, A.; Zimmer, Y.; Yayon, A.; Yarden, Y.; Givol, D.  
Oncogene 6, 1089-1092, 1991  
A:Title: Flg-2, a new member of the family of fibroblast growth factor receptors.  
A:Reference number: A60350; MUID:91296390; PMID:1648703  
A:Accession: A60350  
A:Molecule type: mRNA  
A:Residues: 1-800 <AVI>  
A:Cross-references: EMBL:X58255; NID:G31382; PIDN:CAA41209.1; PID:G31383  
A:Experimental source: keratinocytes  
C:Comment: This may be a receptor for keratinocyte growth factor.  
C:Genetics:  
A:Gene: GDB:FGFR2; JWS; CFD1; KGF; FLG2  
A:Cross-references: GDB:127273; OMIM:176943  
A:Map position: 10q25.3-10q26  
C:Superfamily: basic fibroblast growth factor receptor 1; immunoglobulin homology; prote  
C:Keywords: ATP; autophosphorylation; duplication; glycoprotein; growth factor receptor;  
F:1-31/Domain: signal sequence #status predicted <SIG>  
F:22-800/Product: fibroblast growth factor receptor flg-2 #status predicted <MAT>  
F:22-369/Domain: extracellular #status predicted <EXT>  
F:131-137/Region: acidic  
F:262-335/Domain: immunoglobulin homology <IMM>  
F:370-390/Domain: transmembrane #status predicted <TM>  
F:391-800/Domain: intracellular #status predicted <INT>  
F:464-749/Domain: protein kinase homology <KIN>  
F:472-480/Region: protein kinase ATP-binding motif  
F:59-107,170-222,269-333/Disulfide bonds: #status predicted  
F:96-107,256,288,309,322/Binding site: carbohydrate (Asn) (covalent) #status predicted  
F:502,519,611/Active site: Lys, Glu, Asp #status predicted  
F:616,629/Binding site: magnesium (Asn, Asp) #status predicted  
F:642/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predicted

Query Match 20.7%; Score 453.5; DB 1; Length 800;  
Best Local Similarity 30.5%; Pred. No. 7.8e-16;  
Matches 120; Conservative 71; Mismatches 165; Indels 37; Gaps 9;

QY 34 VTIFLILGLVILWLFIREORTQOORSGPQGIAPV---PPPRDLSEWAGHGNVALPKNET 90  
DB 375 VVFFELFILVAAVILCLRSPKGLGSPVHKVSRFPLKRVQSLSSNMSNTPL--V 432

QY 91 SVENFLGATTPALA---KLQVP-----RQLSEVLEQICSGSGGPIFRANMTGD 137  
DB 433 RIARLSSGEGEVLANVSELELPADPKWELSRTRLTLGKPLGEGCFGVWAAEATGDKDR 492

QY 138 PSKPKSVILKALKEPAGLHEVQDFLGRIOFHYLGKHKNLVQLGECCTEKLPLYMWLEDV 197  
DB 493 TAKEVTVAVMKDDATDKDLSDLVSEWEMWKMKGKHKNIINLLGACTQGGPLVIVEYA 552

QY 198 AQGDLGLFWTCRRDVTMTDGLLY-----DLTEKQVYHIGKQVLLALEFLOEKHL 247  
DB 553 AKGNLREFL--RARRP-----PGMDYSPDACLRLPEQLTKDLVSCAYQVARGMEYLASKC 607

QY 248 FHGDVAARNILMQSDLTAKLGLGLAYEYVTRGAISSSTOT--IPLKWLAPERLLLRPASI 305  
Db 608 IHRDLAARNVLVTEDNVNWKIADFGIARDVHNDIYKKTNGRLPDKVWMAPEALFDRVYTH 667  
QY 306 RADVMSFGILLVEMVTGAPPYVPEVPTSIHLQRRKIMKRPSSCTHTMYIMSKSCRW 365  
Db 668 QSDVMSFGVLLWEIFTLGSSPYGIPVEELFKLLKEGHRMDKPACTHDLVIMRECWHIA 727  
QY 366 READRPSRELRLLE--AAIKTADDAVLQVP 396  
Db 728 VPSQRTFKQLVEDLDRILVTSTDEYLDLSP 760

## RESULT 7

A48991  
heparin-binding growth factor receptor - mouse  
N:Alternate names: HBGF receptor  
N:Contains: protein-tyrosine kinase (EC 2.7.1.112)  
C:Species: Mus musculus (house mouse)  
C:Date: 19-Dec-1993 #sequence\_revision 18-Nov-1994 #text\_change 04-Feb-2000  
C:Accession: A48991  
R:Katoch, O.; Hattori, Y.; Sasaki, H.; Sakamoto, H.; Fujimoto, K.; Fujii, T.; Sugimura, T.  
Cancer Res. 53, 1136-1141, 1993  
A:Title: Isolation of the complementary DNA encoding a mouse heparin-binding growth factor  
A:Reference number: A48991; MUID:93177694; PMID:8382556  
A:Accession: A48991  
A:Status: preliminary  
A:Molecule type: nucleic acid  
A:Residues: 1-800 <KAT>  
A:Cross-references: GB:S56291; NID:G298329; PIDN:AAB25535.1; PID:G298330  
A:Experimental source: brain  
A:Note: sequence extracted from NCBI backbone (NCBI:126536, NCBI:126537)  
C:Superfamily: basic fibroblast growth factor receptor 1; immunoglobulin homology; prote  
C:Keywords: ATP; growth factor receptor; heparin binding; phosphotransferase; tyrosine-s  
F:262-335/Domain: immunoglobulin homology <IMM>  
F:464-749/Domain: protein kinase homology <KIN>  
F:472-480/Region: protein kinase ATP-binding motif

Query Match 20.7%; Score 453.5; DB 2; Length 800;  
Best Local Similarity 30.5%; Pred. No. 7.8e-16;  
Matches 120; Conservative 71; Mismatches 165; Indels 37; Gaps 9;  
QY 34 VTIFILLLGVILWLFIREQRTQOORSGPOGIAPV---PPRDLSEAGHGNVALPLKET 90  
Db 375 VVFFELVVAIVLCRLSPKPKGLGSPVHKVSRFPKRVQVLSNSSMNSNTP--V 432  
QY 91 SVENFLGATTPALA---KLQVP-----REQISEVLEQICSGSCGPIFRANNTGD 137  
Db 433 RIARLSSGEGPVLNVSELEPADPKWLSRSLTLGKPLGEGCGVQVWMAEAGIDKDR 492  
QY 138 PSKPKSVILKALKEPAGLHEVODFLGRIOHQVILGKHNLVQLEGCTEKLPLYMVLVDV 197  
Db 493 TAKPVTVAVMKLDDATDKDLSLVSEMEMMKMIGKHNIINLLGACTQGGLPLYVEYA 552  
QY 198 AQDGLLGLWTCRRDVTMTDGLLY-----DLTEKQVYHIGKQVLLALEFLQEKHL 247  
Db 553 AKGNLREFL-RARRP-----PGMDYSFDACELPEEQLTCKDLVSCAYQVARGMEYLASQKC 607  
QY 248 FHGDVAARNILMQSDLTAKLGLGLAYEYVTRGAISSSTOT--IPLKWLAPERLLLRPASI 305  
Db 608 IHRDLAARNVLVTEDNVNWKIADFGIARDVHNDIYKKTNGRLPDKVWMAPEALFDRVYTH 667  
QY 306 RADVMSFGILLVEMVTGAPPYVPEVPTSIHLQRRKIMKRPSSCTHTMYIMSKSCRW 365  
Db 668 QSDVMSFGVLLWEIFTLGSSPYGIPVEELFKLLKEGHRMDKPACTHDLVIMRECWHIA 727  
QY 366 READRPSRELRLLE--AAIKTADDAVLQVP 396  
Db 728 VPSQRTFKQLVEDLDRILVTSTDEYLDLSP 760

## RESULT 8

## S38579

fibroblast growth factor receptor 3 - Iberian ribbed newt (fragment)  
C:Species: Pleurodeles waltlil (Iberian ribbed newt)  
C:Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 16-Jul-1999  
C:Accession: S38579  
R:Shi, D.L.; Fromentoux, V.; Launay, C.; Umbhauer, M.; Boucaut, J.C.  
submitted to the EMBL Data Library, November 1993  
A:Description: Expression of FGFR-3 in amphibian embryos.  
A:Reference number: S38579  
A:Accession: S38579  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-797 <SHI>  
A:Cross-references: EMBL:X75603  
C:Superfamily: basic fibroblast growth factor receptor 1; immunoglobulin homology; prote  
C:Keywords: ATP; growth factor receptor  
F:258-331/Domain: immunoglobulin homology <IMM>  
F:456-741/Domain: protein kinase homology <KIN>  
F:464-472/Region: protein kinase ATP-binding motif

## Query Match 20.4%; Score 447; DB 2; Length 797;

Best Local Similarity 28.8%; Pred. No. 1.6e-15;  
Matches 112; Conservative 81; Mismatches 166; Indels 30; Gaps 8;  
QY 33 LVTFILLLGVILWLFIREQRTQOORSGPOGIAPVPPRDLSEAGHGNVALPL-KETS 91  
Db 369 VAVVILVVIIFTYKMKVPSKKTMTATVHKVSKFPLKEQVLSNSSMNSNTPLVRIIR 428  
QY 92 VENFLGATTPALAKLQVP-----REQISEVLEQICSGSCGPIFRANNTGDPSKP 141  
Db 429 LSSDGPPLANVSELEPADPKWLSRSLTLGKPLGEGCGVQVWMAEAGIEKDKPNKA 488  
QY 142 KSVILKALKEPAGLHEVODFLGRIOHQVILGKHNLVQLEGCTEKLPLYMVLVDVQGD 201  
Db 489 TSVAVMKLDDATDKDLSLVSEMEMMKMIGKHNIINLLGACTQGGLPLYVEYVASKN 548  
QY 202 LIGFLWTCRRDVTMTDGLLY-----DLTEKQVYHIGKQVLLALEFLQEKHLFHGD 251  
Db 549 LREYL-RARRP-----PGMDYSFDTCLEPEEQLTCKDLVSCAYQVARGMEYLASQKCIHRD 603  
QY 252 VAARNILMQSDLTAKLGLGLAYEYVTRGAISSSTOT--IPLKWLAPERLLLRPASI 309  
Db 604 LAARNVLVTDDNVNWKIADFGIARDVHNDIYKKTNGRLPDKVWMAPEALFDRVYTHQSDV 663  
QY 310 WSEFGLLYVEMVTGAPPYVPEVPTSIHLQRRKIMKRPSSCTHTMYIMSKSCRWREAD 369  
Db 664 WSEFGLLYVEMVTGAPPYVPEVPTSIHLQRRKIMKRPSSCTHTMYIMSKSCRWREAD 369  
QY 370 RPSRELRLLEAAIK-TADDAV-LQVP 396  
Db 724 RPTFKQLVEDLDRILVTSTDEYLDLSP 752

## RESULT 9

A35963  
protein-tyrosine kinase (BC 2.7.1.112) cek2 precursor - chicken  
C:Species: Gallus gallus (chicken)  
C:Date: 09-Nov-1990 #sequence\_revision 09-Nov-1990 #text\_change 16-Jul-1999  
C:Accession: A35963  
R:Pasquale, E.B.  
Proc. Natl. Acad. Sci. U.S.A. 87, 5812-5816, 1990  
A:Title: A distinctive family of embryonic protein-tyrosine kinase receptors.  
A:Reference number: A35963; MUID:90332672; PMID:2165604  
A:Accession: A35963  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-806 <PAS>  
A:Cross-references: GB:M35195; NID:G211442; PIDN:AAA48664.1; PID:G211443  
C:Genetics:  
C:Gene: cek2  
C:Superfamily: basic fibroblast growth factor receptor 1; immunoglobulin homology; prote  
C:Keywords: ATP; autophosphorylation; duplication; glycoprotein; growth factor receptor,  
F:1-23/Domain: signal sequence #status predicted <SIG>

F:24-806/Product: protein-tyrosine kinase cek2 #status predicted <MAT>  
F:24-368/Domain: extracellular #status predicted <EXT>

F:131-138/Region: acidic

F:262-335/Domain: immunoglobulin homology <IMM>

F:369-389/Domain: transmembrane #status predicted <TM>

F:390-806/Domain: intracellular #status predicted <INT>

F:464-749/Domain: protein kinase homology <KIN>

F:472-480/Region: protein kinase ATP-binding motif

F:61-107,170-222,269-333/Disulfide bonds: #status predicted

F:96-219,256,288,309,322/Binding site: carbohydrate (Asn) (covalent) #status predicted

F:502,519,611/Active site: Lys, Glu, Asp #status predicted

F:616,629/Binding site: magnesium (Asn, Asp) #status predicted

F:642/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predicted

Query Match 20.4%; Score 446.5; DB 2; Length 806;  
Best Local Similarity 30.1%; Pred. No. 1.7e-15;  
Matches 118; Conservative 79; Mismatches 164; Indels 31; Gaps 9;

Qy 31 TLLVTIFILGVILWLFIREQRTQQRSQPGIAPVPPR-DLSWEAGHGNGVALPL-K 88

Db 374 TGLVLFILVILVILICRMKPKAMNTTQKVSKEFLKQQVSLSSNNSNTPLVR 433

Qy 89 ETSVENFEGATTALAKLQVP-----REQLSVLEQICSGSCGPIFRANMNTGDP 138

Db 434 ITRUSSGPMANVSELEPPDKWEIARGRLTLGKPLGEGCGQVVMABEIGIDKDKP 493

Qy 139 SKPKSVILKALKEPAGLHEVODFLGRIOFHVGLGKHKNLVOLGCGCTEKLPLYMVLEDA 198

Db 494 NKAITVAVKMKDDATDKDLSLVSEMMKMGKHKNIINLLGACTQGGPLYVLVEYAS 553

Qy 199 QGDLGLFWTCRRDVTMTDGLLY-----DLTEKQVYHIGKQVLLALEFLQEKLH 248

Db 554 KGNLREYL-RARRP----PGMDYSFDCTCKLPEEQLTFCDLVSCAYQVARGMEYLASQKI 608

Qy 249 HGDVAARNILMQSDLTAKLGLGLAYEYVTRGAISSQT--IPLKWLAPERILLRPAISIR 306

Db 609 HRDLAARNVLVTEDNVMKIADFLGARDVHNIIDYKKTNGRLPLVKWMAPEALFDRVYTHQ 668

Qy 307 ADVMSFGILLYEMVTGLAPPYEPVPTSLHLORRKIMKRPSSCTHTMYSMKSCWR 366

Db 669 SDVMSFGVLLWEITFLGSGPFGIPVEELFKLKEGHRMDRPNCTHLYMIMRECWHAV 728

Qy 367 EADRPSPRELRLRLAEAI-KTADDEAV-LQVP 396

Db 729 PSQRPTEFKQLVEDLDRVLTMTSTDEYLDLSVP 760

RESULT 10

I55363

fibroblast growth factor receptor 3 - mouse

C:Species: Mus musculus (house mouse)

C:Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 16-Jul-1999

C:Accession: I55363; B53627

E:Ornitz, D.M.; Leder, P.

J. Biol. Chem. 267, 16305-16311, 1992

A:Title: Ligand specificity and heparin dependence of fibroblast growth factor receptors

A:Reference number: I55363; MUID:92355591; PMID:1379594

A:Accession: I55363

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-801 <RES>

R:Chellaiah, A.T.; McEwen, D.G.; Werner, S.; Xu, J.; Ornitz, D.M.

J. Biol. Chem. 269, 11620-11627, 1994

A:Title: Fibroblast growth factor receptor (FGFR) 3. Alternative splicing in immunoglobulin

A:Reference number: A53627; MUID:94209351; PMID:7512569

A:Accession: B53627

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 242-364 <CHE>

A:Cross-references: GB:L26492

C:Genetics:

A:Gene: mPR3

A;Introns: 304/3; 353/1

C;Superfamily: basic fibroblast growth factor receptor 1; immunoglobulin homology; prote

C;Keywords: ATP; growth factor receptor

F:262-335/Domain: immunoglobulin homology <IMM>

F:464-750/Domain: protein kinase homology <KIN>

F:472-480/Region: protein kinase ATP-binding motif

Query Match 20.3%; Score 444; DB 2; Length 801;

Best Local Similarity 30.5%; Pred. No. 2.3e-15;

Matches 120; Conservative 71; Mismatches 165; Indels 38; Gaps 10;

Qy 34 VTIFILILGVILWLFIREQRTQQRSQPGIAPV---PPPRDLSWEAGHGNGVALPLKET 90

Db 375 VVFFILVAAVILCLRSPKGLGSPVHKVSRFPKLRQVSLSSNNSNTPL--V 432

Qy 91 SVENFLGATTPALA---KLQVP-----RQLSVLEQICSGSCGPIFRANMNTGD 137

Db 433 RIARLSGEGFVLANVSELEPPDKWELSRTRLTLGKPLGEGCGQVVMABEIGIDKDR 492

Qy 138 PSKPSVILKALKEPAGLHEVODFLGRIOFHVGLGKHKNLVOLGCGCTEKLPLYMVLEDA 197

Db 493 TAKPVTAVKMKDDATDKDLSLVSEMMKMGKHKNIINLLGACTQGGPLYVLVEY 552

Qy 198 AQGDLGLFWTCRRDVTMTDGLLY-----DLTEKQVYHIGKQVLLALEFLQEKLH 247

Db 553 AKGNLREYL-RARRP----PGMDYSFDACRLPEEQLTCKDLVSCAYQVARGMEYLASQKC 607

Qy 248 HGDVAARNILMQSDLTAKLGLGLAYEYVTRGAISSQT--IPLKWLAPERILLRPAISIR 305

Db 608 IHRDLAARNVLVTEDNVMKIADFLGARDVHNIIDYKKTNGRLPLVKWMAPEALFDRVYTH 667

Qy 306 RADVMSFGILLYEMVTGLAP--PYEPVPTSLHLORRKIMKRPSSCTHTMYSMKSCWR 364

Db 668 QSDVMSFGVLLWEITFGSGPFGIPVEELFKLKEGHRMDRPNCTHLYMIMRECWH 727

Qy 365 WREADRPSPRELRLRLAE--AAIKTADDEAVLQVP 396

Db 728 AVPSQRPTEFKQLVEDLDRVLTMTSTDEYLDLSVP 761

RESULT 11

TVHUF3

fibroblast growth factor receptor 3 precursor - human

N:Contains: protein-tyrosine kinase (EC 2.7.1.112)

C:Species: Homo sapiens (man)

C:Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 16-Jul-1999

C:Accession: A38576; E58269; I51880

R:Keegan, K.; Johnson, D.E.; Williams, L.T.; Hayman, M.J.

Proc. Natl. Acad. Sci. U.S.A. 88, 1095-1099, 1991

A:Title: Isolation of an additional member of the fibroblast growth factor receptor fami

A:Reference number: A38576; MUID:91142118; PMID:1847508

A:Accession: A38576

A:Molecule type: mRNA

A:Residues: 1-806 <KEE>

R:Cross-references: GB:M58051; NID:g182568; PIDN:AAA52450.1; PID:g182569

R:Thompson, L.M.; Plummer, S.; Schalling, M.; Altherr, M.R.; Gusella, J.F.; Housman, D.E.

Genomics 11, 1133-1142, 1991

A:Title: A gene encoding a fibroblast growth factor receptor isolated from the Huntington

A:Reference number: A55273; MUID:92147110; PMID:1664411

A:Accession: A55273

A:Status: nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 76-394, 'Y', 396-806 <THO>

A:Cross-references: GB:M64347; NID:g182564; PIDN:AAA58470.1; PID:g182565

A>Note: sequence extracted from NCBI backbone (NCBIP:80296)

R:Partanen, J.; Mäkelä, T.P.; Alitalo, R.; Lehto, H.; Alitalo, K.

Proc. Natl. Acad. Sci. U.S.A. 87, 8913-8917, 1990

A:Title: Putative tyrosine kinases expressed in K-562 human leukemia cells.

A:Reference number: A38268; MUID:91062389; PMID:2247464

A:Accession: E38269

A:Molecule type: mRNA

A:Residues: 619-675 <PAR>

A:Cross-references: GB:M37782



R;Bellus, G.A.; Hefferon, T.W.; Ortiz de Luna, R.I.; Hecht, J.T.; Horton, W.A.; Machado, Am. J. Hum. Genet. 56, 368-373, 1995

A;Title: Achondroplasia is defined by recurrent G380R mutations of FGFR3.

A;Reference number: IS1880; MUID:95150025; PMID:7847369

A;Accession: IS1880

A;Status: translated from GB/EMBL/DBDJ

A;Molecule type: DNA

A;Residues: 361-379, 'R', 381-415 <RES>

A;Cross-references: GB:S76733; NID:9914201; PIDN:AAB33323.1; PID:9914202

A;Note: this sequence represents a mutant form associated with achondroplasia

C;Genetics:

A;Gene: GDB:FGFR3

A;Cross-references: GDB:127526; OMIM:100800; OMIM:134934

A;Map position: 4p16.3-4p16.3

C;Function:

A;Description: receptor for both acidic and basic fibroblast growth factors

C;Superfamily: basic fibroblast growth factor receptor 1; immunoglobulin homology; prote

C;Keywords: ATP; autophosphorylation; duplication; glycoprotein; growth factor receptor;

F;1-22/Domain: signal sequence #status predicted <SIG>

F;23-806/Product: fibroblast growth factor receptor 3 #status predicted <MAT>

F;23-375/Domain: extracellular #status predicted <EXT>

F;133-139/Region: acidic

F;268-341/Domain: immunoglobulin homology <IMM>

F;376-396/Domain: transmembrane #status predicted <TM>

F;397-806/Domain: intracellular #status predicted <INT>

F;470-755/Domain: protein kinase homology <KIN>

F;478-486/Region: protein kinase ATP-binding motif

F;61-109,176-228,275-339/Disulfide bonds: #status predicted

F;58,225,262,294,315,328/Binding site: carbohydrate (Asn) (covalent) #status predicted

F;508,525,617/Active site: Lys, Glu, Asp #status predicted

F;622,635/Binding site: magnesium (Asn, Asp) #status predicted

F;648/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predicted

Query Match 20.3%; Score 444; DB 1; Length 806;

Best Local Similarity 30.5%; Pred. No. 2.3e-15;

Matches 117; Conservative 74; Mismatches 161; Indels 32; Gaps 8;

QY 34 VTIFILLLGVILWLFIREQTOOQSGP---QGIAPVPPRLDSWEAGHGNVALPL-KE 89

DB 381 VGFFIFILVAAVTLCLRLSPKGLGSPVTHKISRFPKRVLSNASMSNTPLVRI 440

QY 90 TSVENFLGATTPALAKLOVP-----REQLSEVLQICSGCGPIFRANMTGDP 139

DB 441 ARLSGEGPTLANSELELPADPKWELSRALTGLKPLGEGCFQGVWAAEIGDKDRAA 500

QY 140 KPSVYLKALKEPAGLHEVQDFLGRIOHYLGKKNLVLEGGCTCKLPLYWVLEDAQ 199

DB 501 KPVTAVAVKMLKDDATDKDLSDVSEMEMMKMTGKHKNIINLLGACTQGGPLVLYVEYAAK 560

QY 200 GDLGLFLWTCRRDVTMTDGLLY-----DLTEKQVYHIGKQVLLALEFLQEKHLFH 249

DB 561 GNLREFL-RARP-----PGLDYSFDTCKPEPQLTFKDLVSCAYQVARGMEYLAQKCIH 615

QY 250 GVAARNILMQSDTLAKLGLGLAYEVYTRGAISSTQT--IPKWLAPERLLLRPASTRA 307

DB 616 RDLAARNVLVTDNWKIADFGIARDVHMLDYKKTTNGRLPVKWMAPEALDRVYTHQS 675

QY 308 DWMSGILLIYEMVTIGAPPYVPPTSLIEHLQRRKIMKRPSSCTHMYSIMKSCWRWRE 367

DB 676 DWMSGVLLWEIITLGGSPYGPVVEELFKLKEGHRMDKPNCTHDLIMRECWHAP 735

QY 368 ADPSPRELRLLEAAIK-TADDE 390

DB 736 SQRPYFKQLVEDLRLVITVSTDE 759

RESULT 12

IS0128

fibroblast growth factor receptor - quail

C;Species: Coturnix coturnix (quail)

C;Date: 13-Sep-1996 #sequence\_revision 13-Sep-1996 #text\_change 16-Jul-1999

C;Accession: IS0128; S42803

R;Marcelle, C.; Eichmann, A.; Halevy, O.; Breant, C.; Le Douarin, N.M.

Development 120, 683-694, 1994

A;Title: Distinct developmental expression of a new avian fibroblast growth factor recep

A;Reference number: IS0128; MUID:94215505; PMID:8162862

A;Accession: IS0128

A;Status: preliminary; translated from GB/EMBL/DBDJ

A;Molecule type: mRNA

A;Residues: 1-713 <MAR>

A;Cross-references: EMBL:X76885; NID:9440139; PIDN:CAA54213.1; PID:9440140

C;Genetics:

A;Gene: FREX

C;Superfamily: basic fibroblast growth factor receptor 1; immunoglobulin homology; prote

C;Keywords: ATP; growth factor receptor

F;176-247/Domain: immunoglobulin homology <IMM>

F;377-662/Domain: protein kinase homology <KIN>

F;385-393/Region: protein kinase ATP-binding motif

Query Match 20.1%; Score 439.5; DB 2; Length 713;

Best Local Similarity 29.0%; Pred. No. 3.5e-15;

Matches 131; Conservative 79; Mismatches 163; Indels 79; Gaps 15;

QY 21 EKQYEVITVPT---LLVTIFILLLGVILWLFIREQTOOQSGPQGIAPV-----PP 69

DB 276 EAKYTDIIITSGSLAVAMALII--VVLC-----RMQTQSSKQPLPMAVHKLKSKPL 326

QY 70 PRDLSWEAGHGNVALPLKETSVENFLGATTPALA-----KLVQPREQLSEVL- 117

DB 327 IRQFSLDSSSSGKSTSLMR--VTRLSSSCAPMLAGVVMDDLPLDSKWEPREKL--VLG 382

QY 118 FOICSGSGCPIFRANMTGD---PSKPSVILKALKEPAGLHEVQDFLGRIOHYLGKH 174

DB 383 KPLGEGCFQGVVRAEAYGIDRQWPDRAVTVAVKMLKDNATDKDLADLISEMEMMKLMKDH 442

QY 175 KNLVLEGGCTCKLPLYWVLEDAQDGLLGLFWTCRRDVTMTDGLLYDLTE-----K 226

DB 443 KMINILGVCTQDGLYVIVFAAKGNREYLRA--RRPPTD-YTFDITELHEBQLCFK 499

QY 227 QYVTHGKQVLLALEFLQEKHLFHGDVAARNILMQSDTLAKLGLGLAYEVYTRGAISSTQ 286

DB 500 DLVSCVYQVARGMEYLESRRCIHRDLAARNVLVTAENVKIAADFGLARDVHDIDVYKTS 559

QY 287 T--IPKWLAPERLLLRPASTRADVWSFGILLIYEMVTIGAPPYVPPTSLIEHLQRRKI 344

DB 560 NGRLEPVKWMAPEALDRVYTHQSDVWSFGILMWEITLGGSPYGPVVEELFKLKEGHR 619

QY 345 MKRPSSCTHMYSIMKSCWRWREADRPSPRELRLE---AAIK----- 385

DB 620 WDCPNCTHELIMRECWHAVLPQRPFKQLVEGLDKILAAISREYLDLSMPFEQYSFS 679

QY 386 -----TADDEAVLQVPELVVPELYAAVAG 409

DB 680 CEDTTTSCSDSDSVFTHDPMPLAPCLFSCPSG 711

RESULT 13

TVHUP4

fibroblast growth factor receptor 4 precursor - human

N;Alternate names: protein-tyrosine kinase tkf

N;Contains: protein-tyrosine kinase (EC 2.7.1.112)

C;Species: Homo sapiens (man)

C;Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 16-Jul-1999

C;Accession: S15345; A46615; A41598; D38269

R;Partanen, J.; Maekelae, T.P.; Eerola, E.; Korhonen, J.; Hirvonen, H.; Claesson-Welsh, EMBO J. 10, 1347-1354, 1991

A;Title: FGFR-4, a novel acidic fibroblast growth factor receptor with a distinct expres

A;Reference number: S15345; MUID:91224085; PMID:1709094

A;Accession: S15345

A;Molecule type: mRNA

A;Residues: 1-802 <PAR>

A;Cross-references: EMBL:X57205; NID:g31371; PIDN:CAA40490.1; PID:g31372

A;Note: binds acidic but not basic fibroblast growth factor with high affinity

R;Ron, D.; Reich, R.; Chedid, M.; Lengel, C.; Cohen, O.E.; Chan, A.M.; Neufeld, G.; Mikl

J. Biol. Chem. 268, 5388-5394, 1993

A;Title: Fibroblast growth factor receptor 4 is a high affinity receptor for both acidic



Job time : 21 secs

```
QY 277 YTRGAISSTQTIPLKWLAPERILLRPSAIRADVMSFGILLYEMVTLGAPPYEVPPPTSIL 336
Db 544 TTNG-----RUPVKWMAPEALFDVYTHQSDVMSFGVLMWEIFTLGSGSPYGPVPEELF 597
QY 337 EHLQRRKIMKRPSSCTHTMYSIMKSCWRREADRPSRELRLRLEAAIKTADDEAVLQVP 396
Db 598 KLLKEGHEMDKPTNCTNELYMMRDCWHAVPQSQRPTFKQLVEDLDRLITLTITNEEYLDLT 657
QY 397 E 397
Db 658 Q 658

RESULT 15
A38429
keratinocyte growth factor receptor precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 14-Feb-1992 #sequence_revision 14-Feb-1992 #text_change 16-Jul-1999
C;Accession: A38429
R;Miki, T.; Fleming, T.P.; Bottaro, D.P.; Rubin, J.S.; Ron, D.; Aaronson, S.A.
Science 251, 72-75, 1991
A;Title: Expression cDNA cloning of the KGF receptor by creation of a transforming autoc
A;Reference number: A38429; MUID:91095977; PMID:1846048
A;Accession: A38429
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-707 <MIK>
A;Cross-references: GB:M63503; NID:g198593; PIDN:AAA39377.1; PID:g198594
C;Superfamily: basic fibroblast growth factor receptor 1; immunoglobulin homology; prote
C;Keywords: ATP; autophosphorylation; growth factor receptor; phosphoprotein; transmembr
F;57-118/Domain: immunoglobulin homology <IMM>
F;365-650/Domain: protein kinase homology <KIN>
F;373-381/Region: protein kinase ATP-binding motif

Query Match 19.8%; Score 433; DB 2; Length 707;
Best Local Similarity 27.9%; Pred. No. 7.3e-15;
Matches 118; Conservative 84; Mismatches 165; Indels 56; Gaps 10;

QY 19 IQEKQYEVLIIVPTLL-----VTIFLLILGLVILWLFIREQRTQQQSGSPQGIA----- 65
Db 250 VREK--EITASPDYLEIAIYICIGVFLLIACMVVTVIFCRMKTTTKKPDFSSQPAVHKLTKR 307
QY 66 -PVPPPRDLWSAGHGNNVALPKETSVENFLGATTPALA-----KIQVPREQL 113
Db 308 IPIRQVTVSASSSSMNSNTPLVITLSTADTPMLAGVSEYELPEDPKWEFPRDKL 367
QY 114 SEVLEQICSGSCGPIFRANMNTGDFSPKPK--SVILKALKEPAGLHEVQDFLGRIOFHQY 170
Db 368 T-LGKPLGEGCGQVVMABEAVGIDKDKPKAEVTVAVKMLKDDATEKDLSDLVSEMEMMKM 426
QY 171 LGKHKNLVQLEGCCCTEKLPLYMVLEDAVQGDLLGLFWTCRRDVMTMDGLLYD----- 222
Db 427 IGKHKNIIINLGAQCQDGLYVIVYASKGNLYREYLRARPPGMEYS---YDINRVPEEQ 483
QY 223 LTEKQVYHIGKQVLLALFLOEKHLFHDVAAARNIMQSDLTAKLCGLGLA-----Y 274
Db 484 MTFKDLVSTYQLARGMEYLASQKCIHRDLAARNVLVTENNVMKIADFGIARDINNIDYY 543
QY 275 EYVTRGALSSTQTIPLKWLAPERILLRPSAIRADVMSFGILLYEMVTLGAPPYEVPPPTS 334
Db 544 KKTING-----RLPVKMAPEALFDRVYTHQSDVMSFGVLMWEIFTLGSGSPYGPVPEE 597
QY 335 ILEHLQRRKIMKRPSSCTHTMYSIMKSCWRREADRPSRELRLRLEAAIKTADDEAVLIQ 394
Db 598 LFKLKEGHEMDKPTNCTNELYMMRDCWHAVPQSQRPTFKQLVEDLDRLITLTITNEEYLD 657
QY 395 VPE 397
Db 658 LTQ 660
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Search completed: June 14, 2004, 18:46:17

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 14, 2004, 18:45:49 ; Search time 48 Seconds  
(without alignments)  
2476.842 Million cell updates/sec

Title: US-10-040-884-3  
Perfect score: 2192  
Sequence: 1 MGMTMLLECSLSDKLCVQI.....LYAAVAGIRVESLFYNSML 422

Scoring table: BLOSUM62

Searched: Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters: 1158786

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA:\*

1: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pep.\*  
2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep.\*  
3: /cgn2\_6/ptodata/2/pubpaa/US05\_NEW\_PUB.pep.\*  
4: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pep.\*  
5: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pep.\*  
6: /cgn2\_6/ptodata/2/pubpaa/PCTUS\_PUBCOMB.pep.\*  
7: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB.pep.\*  
8: /cgn2\_6/ptodata/2/pubpaa/US08\_PUBCOMB.pep.\*  
9: /cgn2\_6/ptodata/2/pubpaa/US09A\_PUBCOMB.pep.\*  
10: /cgn2\_6/ptodata/2/pubpaa/US09B\_PUBCOMB.pep.\*  
11: /cgn2\_6/ptodata/2/pubpaa/US09C\_PUBCOMB.pep.\*  
12: /cgn2\_6/ptodata/2/pubpaa/US09\_NEW\_PUB.pep.\*  
13: /cgn2\_6/ptodata/2/pubpaa/US10A\_PUBCOMB.pep.\*  
14: /cgn2\_6/ptodata/2/pubpaa/US10B\_PUBCOMB.pep.\*  
15: /cgn2\_6/ptodata/2/pubpaa/US10C\_PUBCOMB.pep.\*  
16: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB.pep.\*  
17: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep.\*  
18: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2192	100.0	422	14	US-10-040-884-3
2	2188	99.8	458	15	US-10-240-145-67
3	1079	49.2	209	9	US-09-862-027-6
4	542	24.7	104	9	US-09-836-392-24
5	452	20.6	93	9	US-09-864-761-45860
6	444	20.3	806	12	US-10-403-161-58
7	444	20.3	806	15	US-10-394-322A-28
8	444	20.3	808	12	US-10-403-161-60
9	443	20.2	694	16	US-10-302-812-46
10	434	19.8	802	9	US-09-758-386-3
11	434	19.8	802	14	US-10-011-548-33
12	434	19.8	802	14	US-10-354-358-44
13	434	19.8	802	15	US-10-116-275-245
14	434	19.8	802	15	US-10-394-322A-29
15	434	19.8	802	16	US-10-302-812-48

16	432	19.7	822	10	US-09-757-415A-2	Sequence 2, Appli
17	427	19.5	821	15	US-10-394-322A-27	Sequence 27, Appli
18	427	19.5	821	16	US-10-302-812-44	Sequence 44, Appli
19	427	19.5	822	16	US-10-648-593-254	Sequence 254, App
20	424	19.3	735	12	US-10-307-817-6	Sequence 6, Appli
21	424	19.3	764	9	US-09-925-302-714	Sequence 714, App
22	424	19.3	764	12	US-09-925-302-714	Sequence 714, App
23	424	19.3	820	16	US-10-302-812-42	Sequence 42, Appli
24	424	19.3	822	12	US-10-307-817-8	Sequence 8, Appli
25	424	19.3	822	14	US-10-204-041-2	Sequence 2, Appli
26	424	19.3	822	15	US-10-394-322A-26	Sequence 26, Appli
27	424	19.3	824	12	US-10-307-817-4	Sequence 4, Appli
28	422	19.3	1130	14	US-10-204-041-4	Sequence 4, Appli
29	422	19.3	1148	12	US-10-170-385-181	Sequence 181, App
30	422	19.3	1148	16	US-10-408-765A-746	Sequence 746, App
31	421	19.2	650	12	US-10-403-847-116	Sequence 116, App
32	420	19.2	650	14	US-10-193-477-119	Sequence 119, App
33	420	19.2	394	12	US-10-087-192-1131	Sequence 1131, Ap
34	419	19.1	310	9	US-09-939-754-7	Sequence 7, Appli
35	419	19.1	310	9	US-09-939-832-7	Sequence 7, Appli
36	419	19.1	310	9	US-09-939-833-7	Sequence 7, Appli
37	419	19.1	887	15	US-10-258-666-8	Sequence 8, Appli
38	419	19.1	1567	14	US-10-312-918-2	Sequence 2, Appli
39	419	19.1	1594	14	US-10-312-918-4	Sequence 4, Appli
40	418.5	19.1	299	15	US-10-334-143-203	Sequence 203, App
41	417	19.0	1130	12	US-10-276-633-4	Sequence 4, Appli
42	417	19.0	1130	14	US-10-171-889-1	Sequence 1, Appli
43	417	19.0	1130	14	US-10-263-480-2	Sequence 2, Appli
44	417	19.0	1149	15	US-10-457-954-6	Sequence 6, Appli
45	415.5	19.0	891	9	US-09-862-027-25	Sequence 25, Appli

#### ALIGNMENTS

#### RESULT 1

US-10-040-884-3  
; Sequence 3, Application US/10040884  
; Publication No. US2003007822A1  
; GENERAL INFORMATION:  
; APPLICANT: ZENECA Limited  
; TITLE OF INVENTION: HUMAN RECEPTOR TYROSINE KINASE  
; FILE REFERENCE: 70332/US Substantive  
; CURRENT APPLICATION NUMBER: US/10/040,884  
; CURRENT FILING DATE: 2002-01-07  
; PRIOR APPLICATION NUMBER: US/09/310,438  
; PRIOR FILING DATE: 1999-05-28  
; PRIOR APPLICATION NUMBER: US 60/088,958  
; PRIOR FILING DATE: 1998-06-11  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 3  
; LENGTH: 422  
; TYPE: PRT  
; ORGANISM: Homo Sapiens  
US-10-040-884-3

Query Match 100.0%; Score 2192; DB 14; Length 422;  
Best Local Similarity 100.0%; Pred. No. 1.8e-190;  
Matches 422; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGMTMLLECSLSDKLCVQIQEKQYEVIVPTLLVTFILLLGVILWLFIRQRTQQQSSG 60

Db 1 MGMTMLLECSLSDKLCVQIQEKQYEVIVPTLLVTFILLLGVILWLFIRQRTQQQSSG 60

Qy 61 PQGLAPVPPRDLSWEAGHGNNVALPLKETSVENFLGATTTPALAKLQVPRQLSEVLQSI 120

Db 61 PQGLAPVPPRDLSWEAGHGNNVALPLKETSVENFLGATTTPALAKLQVPRQLSEVLQSI 120

Qy 121 CSGSCGPIFRANMNTGDPSPKPSVILKALKEPAGLHEVQDFLGRITQHFQYLGKHNVLQ 180

Db 121 CSGSCGPIFRANMNTGDPSPKPSVILKALKEPAGLHEVQDFLGRITQHFQYLGKHNVLQ 180

QY 181 EGCCTEKLPLYWLEDAQDGLLGLFWTCRRDVTMTDGLLYDLTEKQVYHIGKQVLLALE 240  
DB 181 EGCCTEKLPLYWLEDAQDGLLGLFWTCRRDVTMTDGLLYDLTEKQVYHIGKQVLLALE 240  
QY 241 FLQEKHLFHGDVAARNILMQSDLTAKLGLGLAYEYVTRGAISSTOTIPLKWLAPERLLL 300  
DB 241 FLQEKHLFHGDVAARNILMQSDLTAKLGLGLAYEYVTRGAISSTOTIPLKWLAPERLLL 300  
QY 301 RPASTRADVWSFGILLIYEMVTLGAPPYEVPPPTSILEHLQRRKIMKRPSSCTHTWYSIMK 360  
DB 301 RPASTRADVWSFGILLIYEMVTLGAPPYEVPPPTSILEHLQRRKIMKRPSSCTHTWYSIMK 360  
QY 361 SCWRWREADRPSPRELRLLEAAIKTADDEAVLQVPELVVPELYAAVAGIRVESLFYNS 420  
DB 361 SCWRWREADRPSPRELRLLEAAIKTADDEAVLQVPELVVPELYAAVAGIRVESLFYNS 420  
QY 421 ML 422  
DB 421 ML 422

## RESULT 2

US-10-240-145-67  
; Sequence 67, Application US/10240145  
; Publication No. US20030235883A1  
; GENERAL INFORMATION:  
; APPLICANT: Hyseq, Inc  
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES  
; FILE REFERENCE: 21272-048  
; CURRENT APPLICATION NUMBER: US/10/240,145  
; CURRENT FILING DATE: 2002-09-27  
; PRIOR APPLICATION NUMBER: 09/540,217  
; PRIOR FILING DATE: 2000-03-31  
; PRIOR APPLICATION NUMBER: 09/649,167  
; PRIOR FILING DATE: 2000-08-23  
; PRIOR APPLICATION NUMBER: 09/668,680  
; PRIOR FILING DATE: 2000-09-22  
; PRIOR APPLICATION NUMBER: 09/695,618  
; PRIOR FILING DATE: 2000-10-23  
; PRIOR APPLICATION NUMBER: 09/728,711  
; PRIOR FILING DATE: 2000-11-30  
; PRIOR APPLICATION NUMBER: NOT YET ASSIGNED  
; PRIOR FILING DATE: 2000-03-14  
; NUMBER OF SEQ ID NOS: 172  
; SOFTWARE: Custom  
; SEQ ID NO 67  
; LENGTH: 458  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-240-145-67

Query Match 99.8%; Score 2188; DB 15; Length 458;  
Best Local Similarity 99.8%; Pred. No. 4.5e-190;  
Matches 421; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGMTMLLECSLSDKLCVIOEKQYEVIIPTLAVTIFLILGLVILWFIREQRTQOORSG 60  
DB 37 MGMTMLLECSLSDKLCVIOEKQYEVIIPTLAVTIFLILGLVILWFIREQRTQOORSG 96  
QY 61 PQGIAPVPPRDLTSWEAGHGNVALPLKETSVENFLGATTPALAKLQVPREQLSEVLEQI 120  
DB 97 PQGIAPVPPRDLTSWEAGHGNVALPLKETSVENFLGATTPALAKLQVPREQLSEVLEQI 156  
QY 121 CSGSCGPIFRANMNTGDPSPKSVILKALKEPAGLHVQDFLRIOPHQVILGKHNLVQL 180  
DB 157 CSGSCGPIFRANMNTGDPSPKSVILKALKEPAGLHVQDFLRIOPHQVILGKHNLVQL 216  
QY 181 EGCCTEKLPLYWLEDAQDGLLGLFWTCRRDVTMTDGLLYDLTEKQVYHIGKQVLLALE 240  
DB 217 EGCCTEKLPLYWLEDAQDGLLGLFWTCRRDVTMTDGLLYDLTEKQVYHIGKQVLLALE 276  
QY 241 FLQEKHLFHGDVAARNILMQSDLTAKLGLGLAYEYVTRGAISSTOTIPLKWLAPERLLL 300

DB 277 FLQEKHLFHGDVAARNILMQSDLTAKLGLGLAYEYVTRGAISSTOTIPLKWLAPERLLL 336  
QY 301 RPASTRADVWSFGILLIYEMVTLGAPPYEVPPPTSILEHLQRRKIMKRPSSCTHTWYSIMK 360  
DB 337 RPASTRADVWSFGILLIYEMVTLGAPPYEVPPPTSILEHLQRRKIMKRPSSCTHTWYSIMK 396  
QY 361 SCWRWREADRPSPRELRLLEAAIKTADDEAVLQVPELVVPELYAAVAGIRVESLFYNS 420  
DB 397 SCWRWREADRPSPRELRLLEAAIKTADDEAVLQVPELVVPELYAAVAGIRVESLFYNS 456  
QY 421 ML 422  
DB 457 ML 458

## RESULT 3

US-09-862-027-6  
; Sequence 6, Application US/09862027  
; Patent No. US20020142428A1  
; GENERAL INFORMATION:  
; APPLICANT: Hodge, Martin R.  
; TITLE OF INVENTION: NO. US20020142428A1el Kinases and Uses Thereof  
; FILE REFERENCE: 35800/234862  
; CURRENT APPLICATION NUMBER: US/09/862,027  
; CURRENT FILING DATE: 2001-05-21  
; PRIOR APPLICATION NUMBER: US 09/345,473  
; PRIOR FILING DATE: 1999-06-30  
; NUMBER OF SEQ ID NOS: 82  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 6  
; LENGTH: 209  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-862-027-6

Query Match 49.2%; Score 1079; DB 9; Length 209;  
Best Local Similarity 100.0%; Pred. No. 1e-89;  
Matches 209; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 214 MTMDGLLYDLTEKQVYHIGKQVLLALEFLQEKHLFHGDVAARNILMQSDLTAKLGLGLA 273  
DB 1 MTMDGLLYDLTEKQVYHIGKQVLLALEFLQEKHLFHGDVAARNILMQSDLTAKLGLGLA 60  
QY 274 YEVYTRGAISSTOTIPLKWLAPERLLLRPASIRADVWSFGILLIYEMVTLGAPPYEVPPPT 333  
DB 61 YEVYTRGAISSTOTIPLKWLAPERLLLRPASIRADVWSFGILLIYEMVTLGAPPYEVPPPT 120  
QY 334 SILEHLQRRKIMKRPSSCTHTWYSIMKSCWRWREADRPSPRELRLLEAAIKTADDEAVL 393  
DB 121 SILEHLQRRKIMKRPSSCTHTWYSIMKSCWRWREADRPSPRELRLLEAAIKTADDEAVL 180  
QY 394 QVPELVVPELYAAVAGIRVESLFYNSML 422  
DB 181 QVPELVVPELYAAVAGIRVESLFYNSML 209

## RESULT 4

US-09-836-392-24  
; Sequence 24, Application US/09836392  
; Patent No. US20020173458A1  
; GENERAL INFORMATION:  
; APPLICANT: Ruben et al.  
; TITLE OF INVENTION: Protein Tyrosine Kinase Receptor Polynucleotides, Polypeptides, Antibodies  
; FILE REFERENCE: PT020P1  
; CURRENT APPLICATION NUMBER: US/09/836,392  
; CURRENT FILING DATE: 2001-04-18  
; PRIOR APPLICATION NUMBER: PCT/US00/28066  
; PRIOR FILING DATE: 2000-10-11  
; PRIOR APPLICATION NUMBER: 60/159,542  
; PRIOR FILING DATE: 1999-10-15  
; PRIOR APPLICATION NUMBER: 60/165,914  
; PRIOR FILING DATE: 1999-11-17

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; PRIOR APPLICATION NUMBER: 60/189,027
; PRIOR FILING DATE: 2000-03-14
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 24
; LENGTH: 104
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-836-392-24

Query Match      24.7%; Score 542; DB 9; Length 104;
Best Local Similarity 100.0%; Pred. No. 2.5e-41;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 319 MVTLGAPYPEVPPTSLIEHLQRRKMKRPPSSCTHTMYSIMKSCWRREADRPSRELRL 378
Db 1 MVTLGAPYPEVPPTSLIEHLQRRKMKRPPSSCTHTMYSIMKSCWRREADRPSRELRL 60

QY 379 RLEAAIKTADDEAVLQVPELVVPELYAAVAGIRVESLFYNSML 422
Db 61 RLEAAIKTADDEAVLQVPELVVPELYAAVAGIRVESLFYNSML 104

RESULT 5
US-09-864-761-45860
; Sequence 45860, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharton G.
; APPLICANT: Rank, David R.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aecomica-x-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
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; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 45860
; LENGTH: 93
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC021049.12
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.7
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.75
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.82
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.55
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.64
; OTHER INFORMATION: EST HUMAN HIT: H08599.1, EVALUE 3.00e-05
; OTHER INFORMATION: SWISSPROT HIT: P77580, EVALUE 8.40e-01
US-09-864-761-45860

Query Match      20.6%; Score 452; DB 9; Length 93;
Best Local Similarity 100.0%; Pred. No. 3.3e-33;
Matches 87; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 64 IAPVPPPRDLSEAGHGGNVALPLKETSVENFLGATTPALAKLQVPRQLSEVLEQICSG 123
Db 1 IAPVPPPRDLSEAGHGGNVALPLKETSVENFLGATTPALAKLQVPRQLSEVLEQICSG 60

QY 124 SCGPFIIRANMTGDPSPKPSVILKALK 150
Db 61 SCGPFIIRANMTGDPSPKPSVILKALK 87

RESULT 6
US-10-403-161-58
; Sequence 58, Application US/10403161
; Publication No. US2004004930A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, David et al.
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-573C
; CURRENT APPLICATION NUMBER: US/10/403,161
; CURRENT FILING DATE: 2003-03-31
; PRIOR APPLICATION NUMBER: 60/370349
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/384543
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: 60/370969
; PRIOR FILING DATE: 2002-04-08
; PRIOR APPLICATION NUMBER: 60/403748
; PRIOR FILING DATE: 2002-08-15
; PRIOR APPLICATION NUMBER: 60/372019
; PRIOR FILING DATE: 2002-04-12
; PRIOR APPLICATION NUMBER: 60/374379
; PRIOR FILING DATE: 2002-04-22
; PRIOR APPLICATION NUMBER: 09/779679
; PRIOR FILING DATE: 2001-02-08
; PRIOR APPLICATION NUMBER: 60/181045
; PRIOR FILING DATE: 2000-02-08
; PRIOR APPLICATION NUMBER: 10/055877
; PRIOR FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: 60/262892
; PRIOR FILING DATE: 2001-01-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 173
; SOFTWARE: CuraseqList version 0.1
; SEQ ID NO 58
; LENGTH: 806
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-403-161-58

Query Match      20.3%; Score 444; DB 12; Length 806;
Best Local Similarity 30.5%; Pred. No. 3.4e-31;
Matches 117; Conservative 74; Mismatches 161; Indels 32; Gaps 8;
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QY 34 VTIFLLGLVILWLFIREFQRTQOORSGP---QGIAPVPPPPDLSSWEAGHGNNVALPL-KE 89
Db 381 VGFLLFILVAAVTLCLRLSPKGLGSPVTKISRFPLKQVSLSNASMSNTPLVRI 440
QY 90 TSVENFLGATTPALAKLOVP-----REQLSEVLQICSGSCGPIFRANMTGDP 139
Db 441 ARLSGEGPTLANVSELELPADPKWELSRARLTGLKPLGEGCGQVVMMAEAGIDKDR 500
QY 140 KPKSVILKALKEPAGLHEVQDFLGRIOFHQYLGKHNVLVLEGCCTEKLPLYMVL 199
Db 501 KPTVAVKMLKDDATDKDLSLVSEMMKMGKHNIIINLLGACTQGGGLYVLVYAAK 560
QY 200 GDLGLFWTCRRDVTMDGLLY-----DLTEKQVYHIGKQVLLALEFLQEKH 249
Db 561 GNLREFL-RARRP-----PGLDYSFDTCKPPEEQLTFKDLVSCAYQVARGMEY 615
QY 250 GDAARNILMQSDLTAKLGLGLAYEVYTRGAISSSTQT---IPLKWLAPERLL 307
Db 616 RDLAARNVLVTEDNVNWKIADFGDLARDVHNDLYYKKTNGRLPVKMWAPALF 675
QY 308 DVMSPGILLYEMVTIGAPYEPVPPPTSIIEHLORRKIMKRPSSCTHTMYSIMK 367
Db 676 DVMSPGILLWEIFTLGGSPYGPVBEELFKLKEGHRMDKPNCTHDLIMRECWA 735
QY 368 ADPSPRELRLRLLEAAIK-TADDE 390
Db 736 SQRPTEFKQVLEDLDRVLVTWSTDE 759
RESULT 7
US-10-394-322A-28
; Sequence 28, Application US/10394322A
; Publication No. US20030232391A1
; GENERAL INFORMATION:
; APPLICANT: SUNESIS PHARMACEUTICALS, INC.
; TITLE OF INVENTION: IDENTIFICATION OF KINASE INHIBITORS
; FILE REFERENCE: 39750-0006 US
; CURRENT APPLICATION NUMBER: US/10/394,322A
; CURRENT FILING DATE: 2003-03-20
; PRIOR APPLICATION NUMBER: US 60/366,892
; PRIOR FILING DATE: 2002-03-21
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 28
; LENGTH: 806
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-394-322A-28
Query Match 20.3%; Score 444; DB 15; Length 806;
Best Local Similarity 30.5%; Pred. No. 3.4e-31;
Matches 117; Conservative 74; Mismatches 161; Indels 32; Gaps 8;
QY 34 VTIFLLGLVILWLFIREFQRTQOORSGP---QGIAPVPPPPDLSSWEAGHGNNVALPL-KE 89
Db 381 VGFLLFILVAAVTLCLRLSPKGLGSPVTKISRFPLKQVSLSNASMSNTPLVRI 440
QY 90 TSVENFLGATTPALAKLOVP-----REQLSEVLQICSGSCGPIFRANMTGDP 139
Db 441 ARLSGEGPTLANVSELELPADPKWELSRARLTGLKPLGEGCGQVVMMAEAGIDKDR 500
QY 140 KPKSVILKALKEPAGLHEVQDFLGRIOFHQYLGKHNVLVLEGCCTEKLPLYMVL 199
Db 501 KPTVAVKMLKDDATDKDLSLVSEMMKMGKHNIIINLLGACTQGGGLYVLVYAAK 560
QY 200 GDLGLFWTCRRDVTMDGLLY-----DLTEKQVYHIGKQVLLALEFLQEKH 249
Db 561 GNLREFL-RARRP-----PGLDYSFDTCKPPEEQLTFKDLVSCAYQVARGMEY 615
QY 250 GDAARNILMQSDLTAKLGLGLAYEVYTRGAISSSTQT---IPLKWLAPERLL 307
Db 616 RDLAARNVLVTEDNVNWKIADFGDLARDVHNDLYYKKTNGRLPVKMWAPALF 675
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QY 308 DVMSPGILLYEMVTIGAPYEPVPPPTSIIEHLORRKIMKRPSSCTHTMYSIMK 367
Db 676 DVMSPGILLWEIFTLGGSPYGPVBEELFKLKEGHRMDKPNCTHDLIMRECWA 735
QY 368 ADPSPRELRLRLLEAAIK-TADDE 390
Db 736 SQRPTEFKQVLEDLDRVLVTWSTDE 759
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## RESULT 8

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US-10-403-161-60
; Sequence 60, Application US/10403161
; Publication No. US20040043930A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, David et al.
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-573C
; CURRENT APPLICATION NUMBER: US/10/403,161
; CURRENT FILING DATE: 2003-03-31
; PRIOR APPLICATION NUMBER: 60/370349
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/384543
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: 60/370969
; PRIOR FILING DATE: 2002-04-08
; PRIOR APPLICATION NUMBER: 60/403748
; PRIOR FILING DATE: 2002-08-15
; PRIOR APPLICATION NUMBER: 60/372019
; PRIOR FILING DATE: 2002-04-12
; PRIOR APPLICATION NUMBER: 60/374379
; PRIOR FILING DATE: 2002-04-22
; PRIOR APPLICATION NUMBER: 09/779679
; PRIOR FILING DATE: 2001-02-08
; PRIOR APPLICATION NUMBER: 60/181045
; PRIOR FILING DATE: 2000-02-08
; PRIOR APPLICATION NUMBER: 10/055877
; PRIOR FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: 60/262892
; PRIOR FILING DATE: 2001-01-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 173
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 60
; LENGTH: 808
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-403-161-60
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Query Match 20.3%; Score 444; DB 12; Length 808;
Best Local Similarity 30.5%; Pred. No. 3.4e-31;
Matches 117; Conservative 74; Mismatches 161; Indels 32; Gaps 8;
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QY 34 VTIFLLGLVILWLFIREFQRTQOORSGP---QGIAPVPPPPDLSSWEAGHGNNVALPL-KE 89
Db 381 VGFLLFILVAAVTLCLRLSPKGLGSPVTKISRFPLKQVSLSNASMSNTPLVRI 442
QY 90 TSVENFLGATTPALAKLOVP-----REQLSEVLQICSGSCGPIFRANMTGDP 139
Db 441 ARLSGEGPTLANVSELELPADPKWELSRARLTGLKPLGEGCGQVVMMAEAGIDKDR 502
QY 140 KPKSVILKALKEPAGLHEVQDFLGRIOFHQYLGKHNVLVLEGCCTEKLPLYMVL 199
Db 501 KPTVAVKMLKDDATDKDLSLVSEMMKMGKHNIIINLLGACTQGGGLYVLVYAAK 562
QY 200 GDLGLFWTCRRDVTMDGLLY-----DLTEKQVYHIGKQVLLALEFLQEKH 249
Db 561 GNLREFL-RARRP-----PGLDYSFDTCKPPEEQLTFKDLVSCAYQVARGMEY 617
QY 250 GDAARNILMQSDLTAKLGLGLAYEVYTRGAISSSTQT---IPLKWLAPERLL 307
Db 616 RDLAARNVLVTEDNVNWKIADFGDLARDVHNDLYYKKTNGRLPVKMWAPALF 677
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QY 308 DVWSEFGILLYEMVTGAPPEVPTSLIEHLQRRKIMKRPSSCTHTMYSIMKSCWRWRE 367
Db 678 DVWSEFVLLWELFTLGGSPYGPVPELFLKLLKEGHRMDKPCANTCHDLYMIMRECWAAP 737
QY 368 ADSPSPRELRLRLAAIK-TADDE 390
Db 738 SORPTFKQLVEDLDRVLVTSTDE 761

RESULT 9
US-10-302-812-46
; Sequence 46, Application US/10302812
; Publication No. US20040087016A1
; GENERAL INFORMATION:
; APPLICANT: Keating et al.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR CELL DEDIFFERENTIATION AND
; TISSUE REGENERATION
; FILE REFERENCE: HYDR-P02-004
; CURRENT APPLICATION NUMBER: US/10/302,812
; CURRENT FILING DATE: 2002-11-21
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 46
; LENGTH: 694
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-302-812-46

Query Match 20.2%; Score 443; DB 16; Length 694;
Best Local Similarity 30.7%; Pred. No. 3.4e-31;
Matches 114; Conservative 71; Mismatches 154; Indels 32; Gaps 9;

QY 44 ILWLFIHQRTQQORSQOGIAPVPPPPDLSEAGHGNVALPL-KETSVENFLGATTPA 102
Db 285 IQWL--KHVEVNGSKVGDG-TPVTVLKVSLENASSNTPLVRIARLSSGEGPTLAN 341
QY 103 LAKLQVP-----REQLEVLQICSGSCGPIFRANMNTGDPSPKSVILKALKEP 152
Db 342 VSELELPADPKWELSRARLTGLKPLGEGCFQVVMAEAGIDKRAAKFVTVAVKMLKDD 401
QY 153 AGLHEVQDFLGRIOFHQVGLKHKNLVQLEGCTEKLPLYMVLVDVAQDGLLGFVTCRRD 212
Db 402 ATDKDLSLVSEMEMMKMIGKHKNIINLLGACTQGGLPLYVLEVAAGNLEFL-RARRP 460
QY 213 VMTMDGLLY-----DLTEKQVYHIGKQVLLALEFLQKHLFGCDVAARNILMQSD 262
Db 461 ----PGLDYSFDTCKPPEEQTLTKDLYSCAYQVARGMEYLASQKCIHRDLAARNVLVTE 516
QY 263 LTAKLGLGLAYEYVYTRGAISSTQT--IPLKWLAPERILLRPPASIRADVMSFGILLYEMV 320
Db 517 NVMKIADFGIARDVHNLDDYKKTNGRLPVKMAPEALFDRVYTHQSDVMSFGVLLWEIF 576
QY 321 TLGAPPYEVPTSLIEHLQRRKIMKRPSSCTHTMYSIMKSCWRWREADRPSRELRLRL 380
Db 577 TLGSPYFGIPVEELFKLLKEGHRMDKPCANTCHDLYMIMRECWAAPSQRPTFKQLVEDL 636
QY 381 EAAIK-TADDE 390
Db 637 DRVLVTSTDE 647

RESULT 10
US-09-758-386-3
; Sequence 3, Application US/09758386
; Patent No. US20010016335A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc. et al.
; TITLE OF INVENTION: Fibroblast Growth Factor Receptor-5
; FILE REFERENCE: PF486PCT
; CURRENT APPLICATION NUMBER: US/09/758,386
; CURRENT FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: 09/293,182
; PRIOR FILING DATE: 1999-04-16
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; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 802
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-758-386-3

Query Match 19.8%; Score 434; DB 9; Length 802;
Best Local Similarity 29.8%; Pred. No. 2.7e-30;
Matches 119; Conservative 77; Mismatches 164; Indels 40; Gaps 12;

QY 21 EKQYEVIIV---PTLLVTIFILLGLVILWLFIREQRTQQORSQP-----QGIAPVPPPRDL 73
Db 364 EARTDILLYASGSLAVALLLLAGL-----YRQALHGRHPRPPATVQKLSRFFLARQF 418
QY 74 SWEAGHGNVALPL-KETSVENFLGATTPALAKLQVPREQLSE-----VL-EQICSGSC 125
Db 419 SLESGSGKSSSLVRGVRLLSSGPPALLAGLVSLDLPLDPLWEPRDRDLVLGKPLGEGCF 478
QY 126 GPIFRANMNTGDPSPK---KSVILKALKEPAGLHEVQDFLGRIOFHQVGLKHKNLVQLEG 182
Db 479 GQVVRAEAFGMDFARPDPQASTVAVKMLKONASDKDLADLVSEMEVVKLIGRHKNIINLLG 538
QY 183 CTEKPLMYMVLVDVAQDGLLGFVTCRRDV--MTMDG-----LLYDLTEKQVYHIG 232
Db 539 VCTQEGPLYVIVECAAGNLEFL-RARRPPGDLSPDGPSSSEGLSPFVLVSCAY--- 594
QY 233 KQVLLALEFLQKHLFGCDVAARNILMQSDITAKLGLGLAYEYVYTRGAISSTQT--IPL 290
Db 595 -QVARGMQYLESRKCIHRDLAARNVLVTEDNVMIADFGIARGVHHIDYKKTNGRLPV 653
QY 291 KWLAPERILLRPPASIRADVMSFGILLYEMVTGLGAPPYEVPTSLIEHLQRRKIMKRPSS 350
Db 654 KXMAPEALFDRVYTHQSDVMSFGILLWEIFTLGGSPYFGIPVEELFKLLKEGHRMDRPPH 713
QY 351 CTHMYSIMKSCWRWREADRPSRELRLRLAAIKTADDE 390
Db 714 CPPELYGLMECHWAAPSQRPTFKQLVEALDKVLLVASEE 753

RESULT 11
US-10-011-548-33
; Sequence 33, Application US/10011548
; Publication No. US20030055218A1
; GENERAL INFORMATION:
; APPLICANT: Timans, Jacqueline C.
; Debets, Johannes Eduard Maria
; Antonius
; Sana, Theodore R.
; Bazan, J. Fernando
; Kaselein, Robert A.
; TITLE OF INVENTION: Human Receptor Proteins; Related Reagents and
; Methods
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DNAX Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/011,548
; FILING DATE: 22-Oct-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/173,151
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; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 60/065,776
; FILING DATE: 17-NOV-1997
; APPLICATION NUMBER: US 60/078,008
; FILING DATE: 12-MAR-1998
; APPLICATION NUMBER: US 60/081,883
; FILING DATE: 15-APR-1998
; APPLICATION NUMBER: US 60/095,987
; FILING DATE: 10-AUG-1998
; APPLICATION NUMBER: US 60/078,416
; FILING DATE: 18-MAR-1998
; APPLICATION NUMBER: US 60/062,066
; FILING DATE: 15-OCT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ching, Edwin P.
; REGISTRATION NUMBER: 34,090
; REFERENCE/DOCKET NUMBER: DX0767X
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650)852-9196
; TELEFAX: (650)496-1200
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 802 amino acids
; TYPE: amino acid
; STRANDEDNESS: No. US20030055218A1 Relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 33:
US-10-011-548-33

Query Match 19.8%; Score 434; DB 14; Length 802;
Best Local Similarity 29.8%; Pred. No. 2.7e-30;
Matches 119; Conservative 77; Mismatches 164; Indels 40; Gaps 12;

QY 21 EKQEVILV---PTLLVIFILLGVILWLFIREQTQOORSGP-----QGIAPVPPRDL 73
Db 364 EARYTDIIILYASGSLALAVLLLAGL-----YRQALHGRHPRPPATVQKLSRFFLARQF 418
QY 74 SWEAGHGNNALPL-KETSVENFLGATTPALAKLOVPEOLSE-----VL-EQICSGSC 125
Db 419 SLESGSSGKSSSLVGVRLSSGALLAGLSLDPLDPLWEFFDRDLVLGKPLGEGCF 478
QY 126 GPIFRANMNTGDPKSP---KSVILKALKEPAGLHEVQDFLGRIQHQLGKHNVLQLEG 182
Db 479 GQVRAEAFGMDPARPDQASTAVAKMLKDNASDKDLADLVSEMEVVKLIGRHKNTINLLG 538
QY 183 CTEKLPYLVLEDAVQDGLLGLFWTCRDV---MTMDG-----LLYDLTEKQVYHIG 232
Db 539 VCTQEGPLYVIVECAKGNLREFL-RARRPPGPDLSPDGPRSGEGLSPFVLVSCAY--- 594
QY 233 KOVLLALEPQEKHLFHGDDVAARNILMQSDLTAKLCGLGLAYEVVYTRGAISSTQT--IPL 290
Db 595 -QVARGMQYLESRKCIHRDLARNVLVTEDNVWKIADFGLAGRVHHIDYKKTSNGLPVP 653
QY 291 KWLAPERLLLRPASIRADVWMSFGILLYEMVTIGAPPYEPVPTTSILEHLQRRKIMKRPS 350
Db 654 KWMPEALFDRVYTHQSDVWMSFGILLWEIFTLGGSPYGPVPEELFSLREGHRMDRPPH 713
QY 351 CTHMTYSIMKSCWRWREADRPSRELRLLEAAIKTADDE 390
Db 714 CPPELYGLMRECWAHAPSQRPTFKQLVEALDKVLLAVSEE 753

RESULT 12
US-10-354-358-44
; Sequence 44, Application US/10354358
; Publication No. US20030157082A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc
; APPLICANT: Hunter, John Joseph
; APPLICANT: MacBeth, Kyle J.
; APPLICANT: Tsai, Fong-Ying
; APPLICANT: Lesoon, Andrea
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Db 714 CPPELYGLMRECHWAAPSQRPTFKQLVEALDKVLLAVSEE 753

RESULT 13
US-10-116-275-245
; Sequence 245, Application US/10116275
; Publication No. US20030211476A1
; GENERAL INFORMATION:
; APPLICANT: Elan Pharmaceutical Technology
; APPLICANT: O'Mahony, Daniel J.
; APPLICANT: Brayden, David
; APPLICANT: Byrne, Daragh
; APPLICANT: Lambkin, Imelda
; APPLICANT: Higgins, Lisa
; TITLE OF INVENTION: Genetic Analysis of Peyer's Patches and M Cells and Methods and
; FILE REFERENCE: E1067/20087
; CURRENT APPLICATION NUMBER: US/10/116,275
; CURRENT FILING DATE: 2002-10-04
; NUMBER OF SEQ ID NOS: 349
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 245
; LENGTH: 802
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-116-275-245

Query Match 19.8%; Score 434; DB 15; Length 802;
Best Local Similarity 29.8%; Pred. No. 2.7e-30;
Matches 119; Conservative 77; Mismatches 164; Indels 40; Gaps 12;

QY 21 EKQYEVIIV---PTLLVTIFILGLVILWLFIREQRTQQORSGP----QGIAPVPPPRDL 73
Db 364 EARYTDIILYASGSLALAVLLLAGL-----YRQALHGRHPRPPATVQKLSRFLARQF 418
QY 74 SWEAGHGNVALPL-KETSVENFLGATTPALAKLQVPREQLSE-----VL-EQICSGSC 125
Db 419 SLESGSGKSSSLVRGVRLSSGFPALLAGLVSLDPLDPLWEFFPRDRILVGLKPLGEGCF 478
QY 126 GPIFRANMNTGDPKSP---KSVILKALKEPAGLHEVQDFLGRIOHQHYLVGKHNLVQLEG 182
Db 479 GOVVRAEAFGMDPARPDQAQSTAVVRKMDNADSKDLADLVSEMVKMLIGRHKNIINLLG 538
QY 183 CTEKLPLYMWLEDAQGDLLGLFWTCRRDV---MTMDG-----LLYDLTEKQVYHIG 232
Db 539 VCTQGGPLYVIVECAKGNLREFL-RARRPPGPDLSPPGPRSSGSEGLSPFVLVSCAY--- 594
QY 233 KOVLLALEFLOEKHLFHGDVAARNILMOSDLTAKLCGLGLAYEVYTRGAISSQTQ--IPL 290
Db 595 -QVARGMQYLESRCIKIHRDLAARNVLVTDNVMKIADEFLARGVHHIDYKKTSNGRLPV 653
QY 291 KWLAPERLLRPASTRADVWSFGILLYEMVTLGAPPYEVPTSLILEHLQRRKIMKRPS 350
Db 654 KWAPEALFDRVYTHQSDVWSFGILLWEIIFTLGGSPYGPVPEELFSLREGHRMDRPPH 713
QY 351 CTHMYSIMKSWREADRPSPRELRLLEAAIKTADDE 390
Db 714 CPPELYGLMRECHWAAPSQRPTFKQLVEALDKVLLAVSEE 753

RESULT 15
US-10-302-812-48
; Sequence 48, Application US/10302812
; Publication No. US20040087016A1
; GENERAL INFORMATION:
; APPLICANT: Keating et al.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR CELL DIFFERENTIATION AND
; FILE REFERENCE: HYDR-P02-004
; CURRENT APPLICATION NUMBER: US/10/302,812
; CURRENT FILING DATE: 2002-11-21
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 48
; LENGTH: 802
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-302-812-48

Query Match 19.8%; Score 434; DB 16; Length 802;
Best Local Similarity 29.8%; Pred. No. 2.7e-30;
Matches 119; Conservative 77; Mismatches 164; Indels 40; Gaps 12;

QY 21 EKQYEVIIV---PTLLVTIFILGLVILWLFIREQRTQQORSGP----QGIAPVPPPRDL 73
Db 364 EARYTDIILYASGSLALAVLLLAGL-----YRQALHGRHPRPPATVQKLSRFLARQF 418
QY 74 SWEAGHGNVALPL-KETSVENFLGATTPALAKLQVPREQLSE-----VL-EQICSGSC 125
Db 419 SLESGSGKSSSLVRGVRLSSGFPALLAGLVSLDPLDPLWEFFPRDRILVGLKPLGEGCF 478
QY 126 GPIFRANMNTGDPKSP---KSVILKALKEPAGLHEVQDFLGRIOHQHYLVGKHNLVQLEG 182
Db 479 GOVVRAEAFGMDPARPDQAQSTAVVRKMDNADSKDLADLVSEMVKMLIGRHKNIINLLG 538
QY 183 CTEKLPLYMWLEDAQGDLLGLFWTCRRDV---MTMDG-----LLYDLTEKQVYHIG 232
Db 539 VCTQGGPLYVIVECAKGNLREFL-RARRPPGPDLSPPGPRSSGSEGLSPFVLVSCAY--- 594
QY 233 KOVLLALEFLOEKHLFHGDVAARNILMOSDLTAKLCGLGLAYEVYTRGAISSQTQ--IPL 290
Db 595 -QVARGMQYLESRCIKIHRDLAARNVLVTDNVMKIADEFLARGVHHIDYKKTSNGRLPV 653
QY 291 KWLAPERLLRPASTRADVWSFGILLYEMVTLGAPPYEVPTSLILEHLQRRKIMKRPS 350
Db 654 KWAPEALFDRVYTHQSDVWSFGILLWEIIFTLGGSPYGPVPEELFSLREGHRMDRPPH 713
QY 351 CTHMYSIMKSWREADRPSPRELRLLEAAIKTADDE 390
Db 714 CPPELYGLMRECHWAAPSQRPTFKQLVEALDKVLLAVSEE 753

RESULT 14
US-10-394-322A-29
; Sequence 29, Application US/10394322A
; Publication No. US20030232391A1
; GENERAL INFORMATION:
; APPLICANT: SUNESIS PHARMACEUTICALS, INC.
; APPLICANT: Prescott, John C.
; TITLE OF INVENTION: IDENTIFICATION OF KINASE INHIBITORS
; FILE REFERENCE: 39750-0006 US
; CURRENT APPLICATION NUMBER: US/10/394,322A
; CURRENT FILING DATE: 2003-03-20
; PRIOR APPLICATION NUMBER: US 60/366,892
; PRIOR FILING DATE: 2002-03-21
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Db 479 GOVVAEAFGMDPARPDQASTVAVXMKDNASDKDLADLVSEMEVWKLIGRHKNIINLLG 538  
Qy 183 CTEKLPYMWLEDAQGDLLGFLWTCRRDV---MTMDG-----LLYDLTEKQVYHIG 232  
Db 539 VCTQEGPLYVIVECAAKGNLREFL-RARRPPGDLSPDGPSSSEGPLSPPLVSCAY--- 594  
Qy 233 KOVLLALEFLOEKHLFHGDAARNILMQSDLTAKLCGLGLAYEVYTRGAISSTQT--IPL 290  
Db 595 -QVARGMQYLESKCIHRDLAARNVLVTEEDNVMKIADFGIARGVHHIDYKKTSNGRLPV 653  
Qy 291 KWLAPERILLRPAIRADVWVSFGILLIYEMVTLGAPPYEPVPTSIIEHLQRRKIMKRPSS 350  
Db 654 KWAPEALFDVRYTHQSDVWSFGILLWEIFTLGSGSPYGPVPEELFSLREGHRMDRPPH 713  
Qy 351 CHTHTMYSIMKSWRWREARPSPRELRLEAAIKTADDE 390  
Db 714 CPPELYGLMRECWAAPSORTFKQIWEALDKVLLAVSEE 753

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Job time : 50 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 14, 2004, 18:43:09 ; Search time 22 Seconds  
(without alignments)  
990.280 Million cell updates/sec

Title: US-10-040-884-3

Perfect score: 2192

Sequence: 1 MGMTMLLECSLSDKLCVIQ.....LYAAVAGIRVESLFYNSML 422

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA.\*

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2: /cgn2\_6/ptodata/2/iaa/5B\_COMB.pap.\*

3: /cgn2\_6/ptodata/2/iaa/6A\_COMB.pap.\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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2	444	20.3	801	3	US-09-383-630-6
3	444	20.3	806	3	US-09-383-630-3
4	435	19.8	310	2	US-08-701-191A-8
5	435	19.8	310	4	US-09-664-526-8
6	434.5	19.8	378	1	US-08-070-165F-8
7	434.5	19.8	378	2	US-08-885-418-8
8	434	19.8	802	4	US-09-173-151A-33
9	433	19.8	652	1	US-08-471-570-10
10	427	19.5	821	2	US-08-451-822A-13
11	427	19.5	821	4	US-08-323-430-13
12	424	19.3	729	1	US-07-640-029-3
13	424	19.3	731	1	US-07-921-807B-5
14	424	19.3	731	1	US-08-441-944A-5
15	424	19.3	731	3	US-08-439-992A-3
16	424	19.3	733	1	US-07-640-029-4
17	424	19.3	733	1	US-07-921-807B-6
18	424	19.3	733	1	US-08-441-944A-6
19	424	19.3	733	3	US-08-439-992A-4
20	424	19.3	820	1	US-07-921-807B-3
21	424	19.3	820	1	US-08-441-944A-3
22	424	19.3	820	3	US-08-439-992A-1
23	424	19.3	822	1	US-07-997-133-1
24	424	19.3	822	1	US-07-921-807B-4
25	424	19.3	822	1	US-08-441-944A-4
26	424	19.3	822	2	US-08-451-822A-12
27	424	19.3	822	3	US-08-439-992A-2

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28 424 19.3 822 4 US-08-323-430-12 Sequence 12, Appl
29 423.5 19.3 820 1 US-08-166-717D-6 Sequence 6, Appl
30 423 19.3 769 1 US-08-471-570-8 Sequence 8, Appl
31 422.5 19.3 816 1 US-07-640-029-1 Sequence 1, Appl
32 422 19.3 822 1 US-08-459-296-2 Sequence 2, Appl
33 419 19.1 310 2 US-08-701-191A-1 Sequence 1, Appl
34 419 19.1 310 2 US-08-701-191A-6 Sequence 6, Appl
35 419 19.1 310 4 US-09-390-326-7 Sequence 7, Appl
36 419 19.1 310 4 US-09-664-526-1 Sequence 1, Appl
37 419 19.1 310 4 US-09-664-526-6 Sequence 6, Appl
38 419 19.1 315 2 US-08-701-191A-2 Sequence 2, Appl
39 419 19.1 315 4 US-09-664-526-2 Sequence 3, Appl
40 419 19.1 351 2 US-08-701-191A-3 Sequence 3, Appl
41 419 19.1 351 4 US-09-664-526-3 Sequence 3, Appl
42 418.5 19.1 299 2 US-08-701-191A-13 Sequence 13, Appl
43 418.5 19.1 299 4 US-09-664-526-13 Sequence 13, Appl
44 418.5 19.1 300 2 US-08-701-191A-31 Sequence 31, Appl
45 418.5 19.1 300 4 US-09-664-526-31 Sequence 31, Appl

```

#### ALIGNMENTS

##### RESULT 1

```

US-09-345-473E-6
; Sequence 6, Application US/09345473E
; Patent No. 6558903
; GENERAL INFORMATION:
; APPLICANT: Hodge, Martin
; TITLE OF INVENTION: No. 6558903el Kinases and Uses Thereof
; FILE REFERENCE: 35800/183781
; CURRENT APPLICATION NUMBER: US/09/345,473E
; CURRENT FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 209
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-345-473E-6

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Query Match 49.2%; Score 1079; DB 4; Length 209;
Best Local Similarity 100.0%; Pred. No. 8.2e-91;
Matches 209; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 214 MTMDGLLYDLPTEKQVYHIGKQVLLALEFLQEKHLFHGDDVAARNILMQSDLTAKLGLGLA 273
Db 1 MTMDGLLYDLPTEKQVYHIGKQVLLALEFLQEKHLFHGDDVAARNILMQSDLTAKLGLGLA 60
QY 274 YEVYTRGAISSSTOTPLKWLAPERLLLRPASIRADVMSFGILLYEMVTLGAPPYVEVPPT 333
Db 61 YEVYTRGAISSSTOTPLKWLAPERLLLRPASIRADVMSFGILLYEMVTLGAPPYVEVPPT 120
QY 334 SILEHLQRRKIMKRPSSCTTHMYSIMKSCWRWRADRPSPRELRLLEAAIKTADDEAVL 393
Db 121 SILEHLQRRKIMKRPSSCTTHMYSIMKSCWRWRADRPSPRELRLLEAAIKTADDEAVL 180
QY 394 QVPELVVPELYAAVAGIRVESLFYNSML 422
Db 181 QVPELVVPELYAAVAGIRVESLFYNSML 209

```

##### RESULT 2

```

US-09-383-630-6
; Sequence 6, Application US/09383630A
; Patent No. 6265632
; GENERAL INFORMATION:
; APPLICANT: Avner Yayon et al.
; TITLE OF INVENTION: ANIMAL MODEL FOR FIBROBLAST GROWTH
; FACTOR RECEPTOR ASSOCIATED
; CHONDRODYSPLASIA
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:

```

ADDRESSEE: Mark M. Friedman c/o Anthony Castorina  
STREET: 2001 Jefferson Davis Highway, Suite 207  
CITY: Arlington  
STATE: Virginia  
COUNTRY: United States of America  
ZIP: 22202

## COMPUTER READABLE FORM:

MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk  
COMPUTER: Twinhead\* Slimnote-890TX  
OPERATING SYSTEM: MS DOS version 6.2,  
Windows version 3.11  
SOFTWARE: Word for Windows version 2.0 converted  
to an ASCII file

## CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/383,630A  
Filing DATE: 26-Aug-1999

## CLASSIFICATION: &lt;Unknown&gt;

## PRIOR APPLICATION DATA:

APPLICATION NUMBER: <Unknown>

## FILING DATE: &lt;Unknown&gt;

## ATTORNEY/AGENT INFORMATION:

NAME: Friedman, Mark M.

REGISTRATION NUMBER: 33,883

REFERENCE/DOCKET NUMBER: 1402/2

## TELECOMMUNICATION INFORMATION:

TELEPHONE: 972-3-5625553

TELEFAX: 972-3-5625554

TELEX: <Unknown>

## INFORMATION FOR SEQ ID NO: 6:

## SEQUENCE CHARACTERISTICS:

LENGTH: 801

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 6:

Query Match 20.3%; Score 444; DB 3; Length 801;  
Best Local Similarity 30.5%; Pred. No. 5.6e-32;  
Matches 120; Conservative 71; Mismatches 165; Indels 38; Gaps 10;

QY 34 VTIFLLGVILWLFIREQRTQOQRSGP---PPRDLSEAGHGNVPLKET 90  
DB 375 VVFFILVVAATLCRLSPKGLGSPVHKVSRFPLKQVLSNESMSNSTPL--V 432

QY 91 SVENFLGATTPALA---KLQVP-----REQLSEVLEQICSGSCGPIFRANNTGD 137  
DB 433 RIARLSSGEGPVLAVNSELELPADPKWELSRRLTLGKPLGEGCGQVVMABEIGDKDR 492

QY 138 PSKPKSVILKALKEPAGLHEVQDFLGRIQFHOVLGKHKNLVLEGGCTEKLPLYMVLEDV 197  
DB 493 TAKPVTVAVKMLKDDATDKDLSLVSEMEMMKMIGKHKNIIINLGACTGGPLVLYVEYA 552

QY 198 AGDILGFWTCRRDVTMTDGLLY-----DLTEKQVYHIGKQVLLALEFLOEKHL 247  
DB 553 AKGNLREFL--RARRP---PGMDYSFDACKLPEEQTLTKDLVSCAYQVARGMEYLASQKC 607

QY 248 FHGDVAARNILMQSDLTAKLGLGLAYEYVTRGAISSQT--IPLKWLAPERLLRPASTI 305  
DB 608 IIRDLAARNVLVTEDNVMKIADFGIARDVHNLDDYKKTNGRLPVKMAPEALFORVYTH 667

QY 306 RADVMSFGILLYEMVTLGAP--PYPEVPPTSILEHLQRRKIMKRPSSCTHTMYSIMKSCWR 364  
DB 668 QSDVMSFGVLLWEIFFPGSPSPVPGIPVEELFKLKEGHRMDKPACTHDLIWMRECHW 727

QY 365 WREADRPSPRELRLE--AAIKTADAEVQLVP 396  
DB 728 AVFSORPTKQFVEDLRLITVTSTDEYLDLSVF 761

## RESULT 3

US-09-383-630-3

; Sequence 3, Application US/09383630A

Patent No. 6265632  
GENERAL INFORMATION:  
APPLICANT: Avner Yayon et al.  
TITLE OF INVENTION: ANIMAL MODEL FOR FIBROBLAST GROWTH  
FACTOR RECEPTOR ASSOCIATED  
CHONDRODYSPLASIA

## NUMBER OF SEQUENCES: 18

## CORRESPONDENCE ADDRESS:

ADDRESSEE: Mark M. Friedman c/o Anthony Castorina  
STREET: 2001 Jefferson Davis Highway, Suite 207  
CITY: Arlington  
STATE: Virginia  
COUNTRY: United States of America  
ZIP: 22202

## COMPUTER READABLE FORM:

MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk  
COMPUTER: Twinhead\* Slimnote-890TX  
OPERATING SYSTEM: MS DOS version 6.2,  
Windows version 3.11  
SOFTWARE: Word for Windows version 2.0 converted  
to an ASCII file

## CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/383,630A  
Filing DATE: 26-Aug-1999

## CLASSIFICATION: &lt;Unknown&gt;

## PRIOR APPLICATION DATA:

APPLICATION NUMBER: <Unknown>

## FILING DATE: &lt;Unknown&gt;

## ATTORNEY/AGENT INFORMATION:

NAME: Friedman, Mark M.

REGISTRATION NUMBER: 33,883

REFERENCE/DOCKET NUMBER: 1402/2

## TELECOMMUNICATION INFORMATION:

TELEPHONE: 972-3-5625553

TELEFAX: 972-3-5625554

TELEX: <Unknown>

## INFORMATION FOR SEQ ID NO: 3:

## SEQUENCE CHARACTERISTICS:

LENGTH: 806

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 3:

US-09-383-630-3

Query Match 20.3%; Score 444; DB 3; Length 806;  
Best Local Similarity 30.5%; Pred. No. 5.7e-32;  
Matches 117; Conservative 74; Mismatches 161; Indels 32; Gaps 8;

QY 34 VTIFLLGVILWLFIREQRTQOQRSGP---QGIAPVPPRDLSEAGHGNVPL-KE 89  
DB 381 VGFFILVVAATLCRLSPKGLGSPVHKISRFPLKQVLSNESMSNSTPLVRI 440

QY 90 TSVENFLGATTPALAKLQVP-----REQLSEVLEQICSGSCGPIFRANNTGDPS 139  
DB 441 ARLSGEGPVLAVNSELELPADPKWELSRRLTLGKPLGEGCGQVVMABEIGDKRAA 500

QY 140 KPSVILKALKEPAGLHEVQDFLGRIQFHOVLGKHKNLVLEGGCTEKLPLYMVLEDDVAQ 199  
DB 501 KEPTVAVKMLKDDATDKDLSLVSEMEMMKMIGKHKNIIINLGACTGGPLVLYVEYAAK 560

QY 200 GDLGLFWTCRRDVTMTDGLLY-----DLTEKQVYHIGKQVLLALEFLOEKHLPH 249  
DB 561 GNLREFL--RARRP---PGLDYSFDCKPPEQLTKDLVSCAYQVARGMEYLASQCKIH 615

QY 250 GDVAARNILMQSDLTAKLGLGLAYEYVTRGAISSQT--IPLKWLAPERLLRPASTIRA 307  
DB 616 RDLAARNVLVTEDNVMKIADFGIARDVHNLDDYKKTNGRLPVKMAPEALFDRVYTHQS 675

QY 308 DVMSFGILLYEMVTLGAP--PYPEVPPTSILEHLQRRKIMKRPSSCTHTMYSIMKSCWRRE 367  
DB 676 DVMSFGVLLWEIFFPGSPSPVPGIPVEELFKLKEGHRMDKPACTHDLIWMRECHWAAAP 735

QY 368 ADPSPRELRLLEAAIK-TADDE 390  
 Db 736 SORPTFKQLVEDLDRVLTVTSTDE 759

## RESULT 4

US-08-701-191A-8  
 ; Sequence 8, Application US/08701191A  
 ; Patent No. 5942428  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Moosa Mohammadi, Joseph Schlessinger,  
 ; APPLICANT: and Stevan R. Hubbard  
 ; TITLE OF INVENTION: CRYSTALS OF THE TYROSINE KINASE DOMAIN  
 ; TITLE OF INVENTION: OF NON-INSULIN RECEPTOR TYROSINE KINASE  
 ; NUMBER OF SEQUENCES: 41  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Lyon & Lyon  
 ; STREET: 633 West Fifth Street  
 ; STREET: Suite 4700  
 ; CITY: Los Angeles  
 ; STATE: California  
 ; COUNTRY: U.S.A.  
 ; ZIP: 90071-2066  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
 ; MEDIUM TYPE: Storage  
 ; COMPUTER: IBM Compatible  
 ; OPERATING SYSTEM: IBM P.C. DOS 5.0  
 ; SOFTWARE: Fast-Seq for Windows 2.0  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/701,191A  
 ; FILING DATE: August 21, 1996  
 ; CLASSIFICATION: 530  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER:  
 ; FILING DATE:  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Warburg, Richard J.  
 ; REGISTRATION NUMBER: 32,327  
 ; REFERENCE/DOCKET NUMBER: 227/088  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (213) 489-1600  
 ; TELEFAX: (213) 955-0440  
 ; INFORMATION FOR SEQ ID NO: 8:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 310 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 ; US-08-701-191A-8

Query Match 19.8%; Score 435; DB 2; Length 310;  
 Best Local Similarity 33.4%; Pred. No. 1e-31;  
 Matches 102; Conservative 62; Mismatches 121; Indels 20; Gaps 6;  
 QY 101 PALAKLQVPREQLS--EVLEQICSGSCGPIFRANMNTGDPKPKSVILKALKEPAGLHEV 158  
 Db 11 PADPKWELSRARLTGLKPLGEGCGQVVMABEIGIDKDRRAKPVTVAVKMLKDDATDKDL 70  
 QY 159 QDFLGRIOFHQYLGKHNKLVLEGCCCTEKLPLYMVLEDAQDGLLGFMTCCRDVMTWDG 218  
 Db 71 SDLVSEMEMMKWIGKHNKNIINLLGACTGGGLYVLVEYAAKGNLREFL-RARRP 125  
 QY 219 LLY-----DLTEKQVYHIGKQVLLALEFTLQEKHLPHGDAARNILMQSDLTAKLC 268  
 Db 126 LDYSFDTCKPPEQLTFKDLVSCAYQVARGMEYLASQKCIHRDLAARNVLVTEDNVKIA 185  
 QY 269 GLGLAYEVYTRGAISSQT--IPLKWLAPERLLLRPASIRADVMSFGILLYEMVTLGAPP 326  
 Db 186 DFLGLARDVHNLDDYKKTNGRLPVKWMAPALFDRVYTHQSDVMSFGVLLWEIFTLGGSP 245

QY 327 YPEVPPTSILEHLORRKIMKRPSSCTHTMYSIMKSCWRWREADRPSRELRLLEAAIK- 395  
 Db 246 YPGIPVEELFKLLKEGHRMDKPNCTHDLYMIMRECWMHAAPSQRPTFKQLVEDLDRVLTV 305  
 QY 386 TADDE 390  
 Db 306 TSTDE 310

## RESULT 5

US-09-664-526-8  
 ; Sequence 8, Application US/09664526  
 ; Patent No. 6682921  
 ; GENERAL INFORMATION:  
 ; APPLICANT: MOHAMMADI, MOOSA  
 ; APPLICANT: SCHLESSINGER, JOSEPH  
 ; APPLICANT: HUBBARD, STEVAN R.  
 ; TITLE OF INVENTION: CRYSTALS OF THE TYROSINE KINASE DOMAIN OF NON-INSULIN  
 ; TITLE OF INVENTION: RECEPTOR TYROSINE KINASES  
 ; FILE REFERENCE: 038602/0847  
 ; CURRENT APPLICATION NUMBER: US/09/664,526  
 ; CURRENT FILING DATE: 2000-09-18  
 ; PRIOR APPLICATION NUMBER: 09/188,809  
 ; PRIOR FILING DATE: 1998-11-09  
 ; PRIOR APPLICATION NUMBER: 08/701,191  
 ; PRIOR FILING DATE: 1996-08-21  
 ; NUMBER OF SEQ ID NOS: 41  
 ; SOFTWARE: Patentin Ver. 2.1  
 ; SEQ ID NO 8  
 ; LENGTH: 310  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; US-09-664-526-8

Query Match 19.8%; Score 435; DB 4; Length 310;  
 Best Local Similarity 33.4%; Pred. No. 1e-31;  
 Matches 102; Conservative 62; Mismatches 121; Indels 20; Gaps 6;  
 QY 101 PALAKLQVPREQLS--EVLEQICSGSCGPIFRANMNTGDPKPKSVILKALKEPAGLHEV 158  
 Db 11 PADPKWELSRARLTGLKPLGEGCGQVVMABEIGIDKDRRAKPVTVAVKMLKDDATDKDL 70  
 QY 159 QDFLGRIOFHQYLGKHNKLVLEGCCCTEKLPLYMVLEDAQDGLLGFMTCCRDVMTWDG 218  
 Db 71 SDLVSEMEMMKWIGKHNKNIINLLGACTGGGLYVLVEYAAKGNLREFL-RARRP 125  
 QY 219 LLY-----DLTEKQVYHIGKQVLLALEFTLQEKHLPHGDAARNILMQSDLTAKLC 268  
 Db 126 LDYSFDTCKPPEQLTFKDLVSCAYQVARGMEYLASQKCIHRDLAARNVLVTEDNVKIA 185  
 QY 269 GLGLAYEVYTRGAISSQT--IPLKWLAPERLLLRPASIRADVMSFGILLYEMVTLGAPP 326  
 Db 186 DFLGLARDVHNLDDYKKTNGRLPVKWMAPALFDRVYTHQSDVMSFGVLLWEIFTLGGSP 245  
 QY 327 YPEVPPTSILEHLORRKIMKRPSSCTHTMYSIMKSCWRWREADRPSRELRLLEAAIK- 385  
 Db 246 YPGIPVEELFKLLKEGHRMDKPNCTHDLYMIMRECWMHAAPSQRPTFKQLVEDLDRVLTV 305  
 QY 386 TADDE 390  
 Db 306 TSTDE 310

## RESULT 6

US-08-070-165F-8  
 ; Sequence 8, Application US/08070165F  
 ; Patent No. 5750365  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Chiu, Ing-Ming  
 ; APPLICANT: Poulin, Matthew L  
 ; TITLE OF INVENTION: Acidic Fibroblast Growth Factor (aFGF)  
 ; NUMBER OF SEQUENCES: 12  
 ; CORRESPONDENCE ADDRESS:



ADDRESSEE: Ing-Ming Chiu  
STREET: S2052 Davis Medical Research Center, 480 West  
STREET: 9th Avenue  
CITY: Columbus  
STATE: Ohio  
COUNTRY: USA  
ZIP: 43210

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/070.165F

FILING DATE:  
CLASSIFICATION: 435  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (614)-293-8093  
TELEFAX: (614)-293-5631  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 378 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein

Query Match 19.8%; Score 434.5; DB 1; Length 378;  
Best Local Similarity 32.7%; Pred. No. 1.5e-31;

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101 PALAKLQVPREQLS--EVLQEICSGSCGPIFRANNTGDPKPSVILKALKEPAGLHEV 158
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
27 PADPQWELSRSPITLTKGPIGECFCGQVMDVAVGIEKEKPKNATTVAVMLKDDATKDL 86
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

```

159 QDFLGRIQFHQYLKGKHNVLQLEGCTEKLPLYMWLEDVAQDGLLGFLWTCRRDVTMTDG 218  
97 SLLVSEEMWMTGSKHNTINILGACTONGDPIVLAEVASKGNIRYI-LRARP-----PG 141

87 SUIVSETEHWIWKHKNKINDEBACIQGHIYIVYFPCNKNENLLE AGANE  
219 LIY-----DLTEQVYHGIGVLLALEFLQEHLFGHDVAARNILMQSDLTAKLC 268  
          :  
142 MDYSPTCKLPBEOLTFDOLVCSCAVGMGEYLASORCIHRDLAARLVITDDNNWKA 201

269 GIGLAEVYVTRGAISSQT--IPLKWLAPERLLLPSAIRADVWSFGILLYEMVTLGAPP 326  
|||:|  
202 DFLGRADVENIDYKYKTTGRUPVKKMAPEALFDVYVTHOSDWSFGVLLMEIFLTGSP 261

327 YPEVPPTSILEHLQRRKIMKPSSCTHTWYSIMKSCWRREADRPSRELRLLEAAIK- 385  
|||:::|:  
262 YPGIPIVERFKILKEGRMDKPAANTHELYMIRECWTAVPSORTFFQVDELLDRVLTV 321  
|||:::|:

y	386	TADDEAV-LQVP	396
		:     :	
b	322	TSTDEYLDLSVP	333

RESULT 7  
S-08-885-418-8  
Sequence 8, Application US/08885418  
Patent No. 5925528  
GENERAL INFORMATION:

APPLICANT: Chiu, Ing-Ming  
 APPLICANT: Poulin, Matthew L  
 TITLE OF INVENTION: Acidic Fibroblast Growth Factor (aFGF)  
 NUMBER OF SEQUENCES: 12  
 CORRESPONDENCE ADDRESS:

ADDRESSEE: Ing-Ming Chiu  
STREET: S2052 Davis Medical Research Center, 480 West  
STREET: 9th Avenue  
CITY: Columbus  
STATE: Ohio  
COUNTRY: USA  
ZIP: 43210

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/885,418

FILING DATE:  
 CLASSIFICATION: 435  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (614)-293-8093  
 TELEFAX: (614)-293-5631  
 INFORMATION FOR SEQ ID NO: 8:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 378 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 a-885-418-8

Query Match 19.8%; Score 434.5; DB 2; Length 378;  
Best Local Similarity 32.7%; Pred. No. 1.5e-31;  
Matches 102: Conservative 66; Mismatches 123; Indels 21

Qy	::   :   :   :   :   :   :   :	101 PALAKLVQVPREQLS--EVLEQICSGSCGPIFRANMNTGDPSKPKSVILKALKEPAGLHEV 158
Db	::   :   :   :   :   :   :   :	27 PADPKWELSRSLUTGLKPJEGEGFGGOVVMDAVGIEKEKEPNKATTVAVVMKKDDATDKDL 86

QY 159 QDFLGRIQFHOYLGHKKNLVLEGCTEKIPLYWLEDAQGDLGLFWTCRDDVNTMG 218  
DB 87 SLDVSEEMMKIGIKHIIINLLGACTQDGPYYLYVEAYSGKNLREYL-RARRP-----PG 141

Qy 219 LLY-----DLTEQVYHIGQVLLALEFLQEKHLFHGVDVAARNILMQSDLTAKUC 368

Db 142 MYSFETCKIPREOLTFDVLSCAVQVARGMEYLASOKCHRDIAARNVLVTDNNVMTA 201

269 GGLGAYEVYTRGAISSTQT--IPLKWLAPERLLLRLPASIRADVMSFGILLIYEMVTIGAPP 3266  
202 DFGIARDVHNIDYYKKTNGRLPKVWMAPEALFQVVTTHOSDVMSFGVLLWEFTLGGSP 2611

327	YPEVPTSTLEHLQRRKTKPSSCTHTWYSIMKSCWRREADRPSPRELRLEAAIK-	385
Qy		
262	YPCIPVERIFKLLKRGHMDPAXCTHLYMIMEKCHVAPSORPTKQVSDLRVLTV	321
Db		

Qy	386	TADDEAV-LQVP	396
Dh	322	TSTDYDLSVP	333

RESULT 8  
US-09-173-151A-33  
; Sequence 33, Application US/09173151A

Patent No. 6326472  
GENERAL INFORMATION:  
APPLICANT: Timans, Jacqueline C.  
APPLICANT: Debets, Johannes Eduard Maria  
APPLICANT: Antonius  
APPLICANT: Bana, Theodore R.  
APPLICANT: Bazan, J. Fernando  
APPLICANT: Kastelein, Robert A.  
TITLE OF INVENTION: Human Receptor Prote  
NUMBER OF SEQUENCES: 36  
CORRESPONDENCE ADDRESS:  
ADDRESSES: DNAX Research Institute  
STREET: 901 California Avenue  
CITY: Palo Alto

```

/ STATE: California
/
/ COUNTRY: USA
/
/ ZIP: 94304-1104
/
/ COMPUTER READABLE FORM:
/
/ MEDIUM TYPE: Floppy disk
/
/ COMPUTER: IBM PC compatible
/
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/

```

```

/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/173,151A
/ FILING DATE: 14-OCT-1998
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 60/065,776
/ FILING DATE: 17-NOV-1997
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 60/078,008
/ FILING DATE: 12-MAR-1998
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 60/081,883
/ FILING DATE: 15-APR-1998
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 60/095,987
/ FILING DATE: 10-AUG-1998
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 60/078,416
/ FILING DATE: 18-MAR-1998
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 60/062,066
/ FILING DATE: 15-OCT-1997
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Ching, Edwin P.
/ REGISTRATION NUMBER: 34,090
/ REFERENCE/DOCKET NUMBER: DX0767X
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (650) 852-9196
/ TELEFAX: (650) 496-1200
/ INFORMATION FOR SEQ ID NO: 33:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 802 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: not relevant
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
US-09-173-151A-33

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```

Query Match      19.8%; Score 434; DB 4; Length 802;
Best Local Similarity 29.8%; Pred. No. 4.6e-31;
Matches 119; Conservative 77; Mismatches 164; Indels 40; Gaps 12;

Qy 21 EKQVEIIV---PTLLVTFILILGVILWLFIREQTOQQRSGP-----QGIAPVPPPRDL 73
Db EARVTDIILYASGSLAVALLLAGL-----YRQALHGRHPRPPATVQKLSRFLARQF 418

Qy 74 SWEAGHGNVALPL-KETSVENFLGATTPALAKLOVPREQLSE-----VL-EOICSGSC 125
Db SLESGSGKSSSLVRGVRLSSGFPALLAGLVSLDPLDPLWEFPDRDLVLGKPLGEGCF 478

Qy 126 GPIFRANNTGDPSPK---KSVILKALKEPAGLHEVQDFLGRIOFHOVLGKHVLQLEG 182
Db GOVVRARAFGMDPARPDQASTAVAKMLKDNASDKDLADLVSEMVKMLIGHKNIINLLG 538

Qy 183 CCTKRLPLYMVLVDVAQDGLLGLFWLTCRRDV---MTMDG-----LLYDLTERQVYHIG 232
Db VCTQEGPLYVIVECAAKGNLREEL-RARRPPGPDLSPPGSRSSGCLSPFVLVSCAY--- 594

Qy 233 KOVLLALEFLOEKHLFHGDAARNILMQSDUTAKLCGLGLAYEVYVTRGAISSTOT--IPL 290
Db -QVARGMQYLSRSKCIHRDLAARNVLVTEEDNVMKIADFLARGVHHIDYYKKTSGRLPV 653

Qy 291 KWLAPERLLLPASTRADVWSFGILLYEMVTILGAPPYEVVPTSLILEHQRKMTKRPSS 350
Db KWAPEALFDRVYTHQSDVWSFGILLMEIFTLTGSPYPGIVVEELFSLREGHRMDRPPH 713

Qy 351 CTHMTYSIMKSCWRREADRPSELRLRLLEAAIKTADDE 390
Db CPPELYGLMRCWHAAPSQRFTFKOLVEALDKVLLAVSEE 753

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RESULT 9

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US-08-471-570-10
/ Sequence 10, Application US/08471570
/ Patent No. 5750371
/ GENERAL INFORMATION:
/ APPLICANT: IGARASHI, Koichi
/ APPLICANT: SENOO, Masaharu
/ APPLICANT: WATANABE, Tatsuya
/ TITLE OF INVENTION: PROTEIN, DNA AND USE THEREOF
/ NUMBER OF SEQUENCES: 18
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &
/ ADDRESSEE: CUSHMAN
/ STREET: 130 Water Street
/ CITY: Boston
/ STATE: Massachusetts
/ COUNTRY: US
/ ZIP: 02109
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/471,570
/ FILING DATE: 06-JUN-1995
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US/08/149,664
/ FILING DATE:
/ APPLICATION NUMBER: US 07/743369
/ FILING DATE: 16-AUG-1991
/ ATTORNEY/AGENT INFORMATION:
/ NAME: LINEK, Ernest V
/ REGISTRATION NUMBER: 29822
/ REFERENCE/DOCKET NUMBER: 40897
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (617) 523-3400
/ TELEFAX: (617) 523-6440
/ TELEX: 200291 STRE UR
/ INFORMATION FOR SEQ ID NO: 10:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 652 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
US-08-471-570-10

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Query Match      19.8%; Score 433; DB 1; Length 652;
Best Local Similarity 28.0%; Pred. No. 4.3e-31;
Matches 115; Conservative 82; Mismatches 162; Indels 52; Gaps 9;

Qy 22 KQVEIIVPTLL-----VTIFLILGVILWLFIREQTO-----QQQRSGPQGIAPVPP 69
Db REKEITASPDLTAIYICIGVFLIACMVTVILCRMKNNTKKPDFSQPAVHKLTKRIPL 310

Qy 70 PRDLSWAGHGNVALPLKETSVENFLGATTPALA-----KLOVPREQLSEVLE 118
Db RRQVSASSSSMSNTPFLVRIITLSTADTPMLAGVSEYELPDPKPWEPRDKLT-IGK 369

Qy 119 QICSGSGCPIFRANNTGDPSPK---SVILKALKEPAGLHEVQDFLGRIOFHOVLGKH 175
Db PLGSGCGQVVMFAEAVGIDKDKPEAVTVAVKMLKDDATEKDLSDLVSEMMKMIKHK 429

Qy 176 NLVLEGCCTEKPLPLYMVLVDVAQDGLLGLFWLTCRRDVTMDGLLYD-----LTEKQ 227
Db NIINLLGACTQDGLPLYVIVEYASKGNLREYLARRPPGMEYS---YDINRVPEEQMTFKD 486

Qy 228 VYHIGKQVLLALEFLOEKHLFHGDAARNILMQSDUTAKLCGLGLA-----YEVYTR 279
Db IVSCTYQLARGMEYLAQKCIHRDLAARNVLVTEENVMKTIADFLGARDINNIDYKKTNN 546

Qy 280 GAISSTQTIPLKWLAPERLLLPASTRADVWSFGILLYEMVTILGAPPYEVVPTSLILEHL 339

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Db 547 G-----RLPVKMAPEALFDRVYTHQSDVMSFGVLMWEFTLGGSPYGPVPEELFKLL 600  
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Db 601 KEGHRMDKPAFNTNLYMMRDCWHA VPSQRTFKQLVEDLRLTLTTNE 651

RESULT 10  
US-08-451-822A-13  
; Sequence 13, Application US/08451822A  
; Patent No. 5863888  
; GENERAL INFORMATION:  
; APPLICANT: Dionne, Craig A  
; APPLICANT: Crumley, Greg  
; APPLICANT: Jaye, Michael C  
; APPLICANT: Schlessinger, Joseph  
; TITLE OF INVENTION: Fibroblast Growth Factor Receptors  
; NUMBER OF SEQUENCES: 19  
; CORRESPONDENCE ADDRESS:  
; ADDRESSER: Rhone-Poulenc Rorer Legal Department  
; STREET: 500 Arcola Road  
; CITY: Collegeville  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 19426

COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/451,822A  
; FILING DATE: 26-MAY-1995  
; CLASSIFICATION: 435

PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/323,430  
; FILING DATE: 14-OCT-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/934,372  
; FILING DATE: 21-AUG-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/549,587  
; FILING DATE: 06-JUL-1990  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Savitzky, Martin  
; REGISTRATION NUMBER: 29,699  
; REFERENCE/DOCKET NUMBER: A0496E  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (610) 454-3816  
; TELEFAX: (610) 454-3808  
; INFORMATION FOR SEQ ID NO: 13:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 821 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-451-822A-13

Query Match 19.5%; Score 427; DB 2; Length 821;  
Best Local Similarity 27.4%; Pred. No. 2.1e-30;  
Matches 115; Conservative 84; Mismatches 167; Indels 54; Gaps 9;

QY 22 KOYEVIIVPTLL-----VTIFLLGLVILWLFIREFORTQOORSGPQGLA-----PV 67  
Db 365 REKEIVASPDYLEIAYICGVFLIACWVTVILCRMKNYTKKPDFSQPAVHKLTIRPL 424  
QY 68 PPRDLISWAGHGNVALPKETSVENFLGATTPALA-----KLQVPEQLSEV 116  
Db 425 RRQVTVSAESSSSMNSNTPLVRITRISSTADTPMLAGVSEYELPDKWEPDRDKLT-L 483  
QY 117 LEQICSGSCGPIFRANNTGDDPKPK---SVILKALKEPAGLHEVDLGRIOFHQLGK 173

Db 484 GKPLGEGCGQVWAAEAVGIDKDKPEAVTVAVKMLKDDATEKOLSDLVSEMMKMIGK 543  
QY 174 HKNLVQLBGCCTEKLPLYMVLVEDVAQDGLLGLFWTCRRDVMTMDGLLYD-----LTE 225  
Db 544 HKNINLIGACTQDGLYVIVEYASKGNLREYLRRRPPGMEYS-----YDINRVPEEQMTF 600  
QY 226 KOYVHIGKQVLLALEFLEQEKHLFHGDVAARNILMOSDLTAKLCLGLA-----YEVY 277  
Db 601 KDLVSVCTYQLARGMEYLASQKCIHRDLAARNVLVTENNVMKIADFLGLARDINNIDYKKT 660  
QY 278 TRGAISSTQTIPLKWLAPERLLLRPASTRADVMSFGILLYEMVTLGAPYPVPEVPTSL 337  
Db 661 TNG-----RLPVKMAPEALFDRVYTHQSDVMSFGVLMWEFTLGGSPYGPVPEELFK 714  
QY 338 HLOREKIMKRPSSCTHTMYIMSKSWRREADRPSPRELRLRLLEAAIKTADDEAVLQVPE 397  
Db 715 LLKEGHRMDKPAFNTNLYMMRDCWHA VPSQRTFKQLVEDLRLTLTTNEEYLDLSQ 774

RESULT 11  
US-08-323-430-13  
; Sequence 13, Application US/08323430  
; Patent No. 6344546  
; GENERAL INFORMATION:  
; APPLICANT: Dionne, Craig A  
; APPLICANT: Crumley, Greg  
; APPLICANT: Jaye, Michael C  
; APPLICANT: Schlessinger, Joseph  
; TITLE OF INVENTION: Fibroblast Growth Factor Receptors  
; NUMBER OF SEQUENCES: 15  
; CORRESPONDENCE ADDRESS:  
; ADDRESSER: Rhone-Poulenc Rorer Legal Department  
; STREET: 500 Arcola Road  
; CITY: Collegeville  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 19426

COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/323,430  
; FILING DATE:  
; CLASSIFICATION: 435

PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US to be assigned  
; FILING DATE: 21-AUG-1992  
; APPLICATION NUMBER: US 07/549,587  
; FILING DATE: 06-JUL-1990  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Goodman, Rosanne  
; REGISTRATION NUMBER: 32,534  
; REFERENCE/DOCKET NUMBER: A0496  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (215) 454-3817  
; TELEFAX: (215) 454-3808  
; INFORMATION FOR SEQ ID NO: 13:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 821 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-323-430-13

Query Match 19.5%; Score 427; DB 4; Length 821;  
Best Local Similarity 27.4%; Pred. No. 2.1e-30;  
Matches 115; Conservative 84; Mismatches 167; Indels 54; Gaps 9;  
QY 22 KOYEVIIVPTLL-----VTIFLLGLVILWLFIREFORTQOORSGPQGLA-----PV 67





Qy	147	KALKEPAGLHEVQDFLGRIOFHOYLGKHKNLVOLFEGCCTEKLPYMWLEDAQGDLLGFL	206
Db	423	KWLKSDATEKDLSDLISEMWMKMGKKNIIINLLGACTQDGPLYIVIEYASKGNREYL	482
Qy	207	WTCRRDVTMDGLLY-----DLTEKQVYHIGKQVLLALEFLOEKHLFHGDVAARN	256
Db	483	QARR-----PPGLEVCYNPSHNPERQLSSKDLVSCAYQVARGMEYLASKKCIHRDLAARN	537
Qy	257	ILMQSDLTAKLCLGLAYEVYTRGAISSTOT--IFLKWLAPELRLLRPASIRADVWSFGI	314
Db	538	VLVTEDNVMKIADFLGARDIHHIDYKYKTTNGRLEVKWMAPEALFDRIYTHQSDVWSFGV	597
Qy	315	LLYEMVTLGAPPYEPVPPTSILEHLQRRKIMKRPSSTHTMYSIMKSCWRWREADRPSPR	374
Db	598	LLWEFTLGGSPYGPVPVEELFKLLKEGHRMDKPSNCTNELYMMNRDCWHAVPSORPTEK	657
Qy	375	EIRLRLAAIKTADDEAVIQV	395
Db	658	QLVEDLDRIVALTSNQEYLDL	678

Search completed: June 14, 2004, 18:46:52  
Job time : 23 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 14, 2004, 18:37:48 ; Search time 58 Seconds  
(without alignments)  
2055.777 Million cell updates/sec

Title: US-10-040-884-3  
Perfect score: 2192  
Sequence: 1 MGMTMLLECSLDKLCVQ.....LYAAVAGIRVESLFYNSML 422

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A Geneseq 29Jan04: \*  
1: Geneseqp1980s: \*  
2: Geneseqp1990s: \*  
3: Geneseqp2000s: \*  
4: Geneseqp2001s: \*  
5: Geneseqp2002s: \*  
6: Geneseqp2003as: \*  
7: Geneseqp2003bs: \*  
8: Geneseqp2004s: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2192	100.0	422	3	AAy44297 Human rec
2	2192	100.0	495	4	AAb65706 Novel pro
3	2189	99.9	422	3	AAy44299 Human rec
4	2188	99.8	458	4	AaU68537 Human nov
5	2183	99.6	422	4	AAG66404 Human fib
6	2176.5	99.3	421	3	AAy44298 Human rec
7	1079	49.2	209	4	AB66603 Human h14
8	743	33.9	183	4	AB65707 Novel pro
9	542	24.7	104	4	AAE00672 Human h14
10	452	20.6	93	4	AB433239 Peptide #
11	452	20.6	93	4	AAm37079 Peptide #
12	452	20.6	93	4	AAm76972 Human bon
13	452	20.6	93	4	ABG58633 Human liv
14	452	20.6	93	4	AAE21977 Mouse fib
15	444	20.3	801	4	ABj38646 Human fib
16	444	20.3	806	6	ABj38646 Human fib
17	444	20.3	806	6	ADA89050 Human FGF
18	444	20.3	806	6	AAE36462 Human FGF
19	444	20.3	806	6	ABG66739 Human nov
20	443	20.2	694	5	AAr15269 Clone pTB
21	435	19.8	652	2	AAy06456 ZNF198-FG
22	435	19.8	687	2	AAy06456 Fibroblas
23	434.5	19.8	378	2	AAW37805 Newt fibr
24	434.5	19.8	378	2	AAE16588 Human fib
25	434	19.8	802	5	AAE16588 Human fib

## ALIGNMENTS

RESULT 1									
AAy44297									
ID	AAy44297	standard; protein; 422 AA.	802	6	ABR58627	Human can	19.8	434	26
XX	XX		802	7	ADB31984	Human fib	19.8	434	27
AC	AAy44297;		802	7	ADE58199	Human Pro	19.8	434	28
XX	XX		802	7	ADE58203	Human Pro	19.8	434	29
DT	29-FEB-2000	(first entry)	802	7	ADE58195	Human Pro	19.8	434	30
XX	XX		802	7	ADE58207	Human Pro	19.8	434	31
DE	Human receptor tyrosine kinase.		802	7	ADE38383	Human Pro	19.8	434	32
XX	XX		822	4	AAU04694	Mouse fib	19.7	432	33
KW	Human; receptor tyrosine kinase; RTK; tyrosine kinase modulator;		731	2	AAU04694	Mouse fib	19.6	430	34
KW	signal transduction tyrosine kinase; Cdc2 kinase; mitosis; tumour;		821	7	ADE57113	Human bFG	19.5	427	35
KW	cancer; adenocarcinoma; brain; Alzheimer; RTK associated disorder;		821	7	ADD45446	Human Pro	19.4	426	36
KW	adenocarcinoma; angiogenesis; arthritis; diabetic retinopathy;		1130	6	ABU10189	Human Pro	19.4	426	37
KW	ischaemic heart disease; atherosclerosis; inflammation.		1130	6	ABG76260	Human mut	19.3	424	38
XX	XX		731	2	AAr10649	Human Bcr	19.3	424	39
OS	Homo sapiens.		764	3	AAr58376	Chicken b	19.3	424	40
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FT	Domain	1..122							
FT	FT	/label= Non-kinase domain							
FT	FT	/note= "can be used as a dominant negative form for screening therapeutic compounds"							
FT	Domain	1..25							
FT	FT	/label= Extracellular domain							
FT	FT	/note= "can be used for screening therapeutic compounds"							
FT	FT	26..422							
FT	FT	/label= Cytoplasmic domain							
FT	FT	/note= "intracellular functional domain which can be used for screening therapeutic compounds"							
FT	Domain	123..422							
FT	FT	/label= Tyrosine kinase domain							
FT	FT	/note= "can be used for screening therapeutic compounds"							
XX	XX	WO9964589-A1.							
XX	XX	16-DEC-1999.							
PD	PD	08-JUN-1999; 99WO-GB001798.							
PF	PF	11-JUN-1998; 98US-0088958P.							
XX	XX	(ZENE ) ZENECA LTD.							
XX	XX	Gildyal N, Panchamoorthy G;							
XX	XX	WPI; 2000-097538/08.							
DR	DR	N-PSDB; AAZ29332, AAZ29331.							

XX New nucleic acid encoding human tyrosine kinase, overexpressed in, e.g.  
PT cancers for treating adenocarcinoma.  
XX  
XX  
PS Claim 11; Page 49-50; 56pp; English.  
XX  
XX The present sequence is a human receptor tyrosine kinase (RTK) which  
CC activates Cdc2 kinase that mediates mitosis. Tyrosine kinase is  
CC selectively expressed in human forebrain. It is overexpressed in large  
CC number of carcinomas (e.g. adenocarcinoma) and brain tissues of Alzheimer  
CC patients. Dominant negative mutants derived from the RTK act as tyrosine  
CC kinase modulators. The sequence is used to identify compounds that  
CC modulate biological and/or pharmacological activity of tyrosine kinase  
CC and hence regulate cellular and tissue physiology. The present sequence  
CC and the modulators of tyrosine kinase are used for treating many diseases  
CC related to or mediated by RTK e.g. adenocarcinomas, angiogenesis,  
CC arthritis, diabetic retinopathy, ischaemic heart disease,  
CC atherosclerosis, inflammation, solid tumours and metastases  
XX  
SQ Sequence 422 AA;  
Query Match 100.0%; Score 2192; DB 3; Length 422;  
Best Local Similarity 100.0%; Pred. No. 8.2e-215;  
Matches 422; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MGTRMLLECSLSDKLCVIOEKQYEVIIPTLLVTIFLLGLVILMFIREQTOOQSG 60  
Db 1 MGTRMLLECSLSDKLCVIOEKQYEVIIPTLLVTIFLLGLVILMFIREQTOOQSG 60  
QY 61 PQGIAPVPPRDLSEAGHGNNALPKETSVENFLGATTPALAKLQVPRQLSEVLEQI 120  
Db 61 PQGIAPVPPRDLSEAGHGNNALPKETSVENFLGATTPALAKLQVPRQLSEVLEQI 120  
QY 121 CSGSGPIFRANMNTGDPSPKSVILKALKEPAGLHEVQDFLGRIOPHQYLGKHKNLVQL 180  
Db 121 CSGSGPIFRANMNTGDPSPKSVILKALKEPAGLHEVQDFLGRIOPHQYLGKHKNLVQL 180  
QY 181 EGCCTEKLPLYWVLEDAQGLLGFMTCCRRDVTMDGLLYDLTEKQVYHIGKQVLLALE 240  
Db 181 EGCCTEKLPLYWVLEDAQGLLGFMTCCRRDVTMDGLLYDLTEKQVYHIGKQVLLALE 240  
QY 241 FLOEKHLPHGDVAAARNILMQSDLTAKLCGLGLAYEVYTRGAISSQTQIPLKWLAPERLLL 300  
Db 241 FLOEKHLPHGDVAAARNILMQSDLTAKLCGLGLAYEVYTRGAISSQTQIPLKWLAPERLLL 300  
QY 301 RPASIRADVWSFGILLYEMVTGAPPYEPVPTTSILEHLQRRKIMKRPSSCTHTMYSIMK 360  
Db 301 RPASIRADVWSFGILLYEMVTGAPPYEPVPTTSILEHLQRRKIMKRPSSCTHTMYSIMK 360  
QY 361 SCWRREADRPSRELRLRLAAIKTADDEAVIQVPELVPELYAAVAGIRVESLIFYNS 420  
Db 361 SCWRREADRPSRELRLRLAAIKTADDEAVIQVPELVPELYAAVAGIRVESLIFYNS 420  
QY 421 ML 422  
Db 421 ML 422  
RESULT 2  
AAB65706  
ID AAB65706 standard; protein; 495 AA.  
XX  
XX AAB65706;  
XX  
XX 27-MAR-2001 (first entry)  
DT  
DE Novel protein kinase, SEQ ID NO: 235.  
XX  
XX Human; mouse; protein kinase; antiarthritic; antisclerotic; osteopathic;  
KW immunosuppressive; cardiac; renal; antiinflammatory; antiasthmatic;  
KW dermatological; antidiabetic; antifertility; gene therapy; vaccine;  
KW immune disorder; cardiovascular disease; neurodegenerative disease;  
KW cancer; autoimmune disorder; stroke; inflammatory bowel disease;  
KW

KW inflammatory pelvic disease; multiple sclerosis; psoriasis.  
XX Homo sapiens.  
XX WO200073469-A2.  
XX  
XX 07-DEC-2000.  
XX  
XX 26-MAY-2000; 2000WO-US014842.  
XX  
XX 28-MAY-1999; 99US-0136503P.  
XX (SUGEN-) SUGEN INC.  
XX Plowman GD, Martinez R, Whyte D, Sudersanam S;  
PI WPI; 2001-032161/04.  
XX N-PSDB; AAF44735.  
XX  
XX Nucleic acids encoding kinase polypeptides, useful for diagnosing and  
PT treating immune-related diseases and disorders, cardiovascular disease,  
PT neurodegenerative diseases and/or cancers.  
XX  
XX Claim 10; Fig 1; 310pp; English.  
XX  
XX The present sequence is a novel protein kinase. The novel protein kinases  
CC and the nucleic acids that encode them may be used in the treatment and  
CC diagnosis of diseases associated with inappropriate kinase expression  
CC such as immune-related diseases and disorders, cardiovascular disease,  
CC neurodegenerative diseases and/or cancers. The nucleic acids and  
CC complementary sequences may also be used as DNA probes in diagnostic  
CC assays. The kinase polypeptides may be used as antigens in the production  
CC of antibodies of kinase expression and activity. Anti-kinase antibodies  
CC and kinase antagonists may also be used to down regulate kinase  
CC expression and activity. Diseases related to kinase expression and  
CC activity include rheumatoid arthritis, atherosclerosis, autoimmune  
CC disorders, complications of organ transplantation, myocardial infarction,  
CC immune disorders, cardiomyopathies, strokes, renal failure, oxidative-  
CC stress related disorders, chronic inflammatory bowel disease, chronic  
CC inflammatory pelvic disease, multiple sclerosis, asthma, osteoarthritis,  
CC psoriasis, rhinitis, autoimmunity, diabetes, cancers and reproductive  
CC disorders  
XX  
SQ Sequence 495 AA;  
Query Match 100.0%; Score 2192; DB 4; Length 495;  
Best Local Similarity 100.0%; Pred. No. 1e-214;  
Matches 422; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MGTRMLLECSLSDKLCVIOEKQYEVIIPTLLVTIFLLGLVILMFIREQTOOQSG 60  
Db 74 MGTRMLLECSLSDKLCVIOEKQYEVIIPTLLVTIFLLGLVILMFIREQTOOQSG 133  
QY 61 PQGIAPVPPRDLSEAGHGNNALPKETSVENFLGATTPALAKLQVPRQLSEVLEQI 120  
Db 134 PQGIAPVPPRDLSEAGHGNNALPKETSVENFLGATTPALAKLQVPRQLSEVLEQI 193  
QY 121 CSGSGPIFRANMNTGDPSPKSVILKALKEPAGLHEVQDFLGRIOPHQYLGKHKNLVQL 180  
Db 194 CSGSGPIFRANMNTGDPSPKSVILKALKEPAGLHEVQDFLGRIOPHQYLGKHKNLVQL 253  
QY 181 EGCCTEKLPLYWVLEDAQGLLGFMTCCRRDVTMDGLLYDLTEKQVYHIGKQVLLALE 240  
Db 254 EGCCTEKLPLYWVLEDAQGLLGFMTCCRRDVTMDGLLYDLTEKQVYHIGKQVLLALE 313  
QY 241 FLOEKHLPHGDVAAARNILMQSDLTAKLCGLGLAYEVYTRGAISSQTQIPLKWLAPERLLL 300  
Db 314 FLOEKHLPHGDVAAARNILMQSDLTAKLCGLGLAYEVYTRGAISSQTQIPLKWLAPERLLL 373  
QY 301 RPASIRADVWSFGILLYEMVTGAPPYEPVPTTSILEHLQRRKIMKRPSSCTHTMYSIMK 360  
Db 374 RPASIRADVWSFGILLYEMVTGAPPYEPVPTTSILEHLQRRKIMKRPSSCTHTMYSIMK 433

QY 361 SCWRREADRPSPRELRLLEAAIKTADDEAVLQVPELVPELYAAVAGIRVESLFYNYS 420  
 Db 434 SCWRREADRPSPRELRLLEAAIKTADDEAVLQVPELVPELYAAVAGIRVESLFYNYS 493  
 QY 421 ML 422  
 Db 494 ML 495

RESULT 3  
 ID AAY44299 standard; protein; 422 AA.  
 AC AAY44299;  
 XX  
 XX 29-FEB-2000 (first entry)  
 DT Human receptor tyrosine kinase dominant negative mutant-2.  
 DE  
 DE Human; receptor tyrosine kinase; RTK; tyrosine kinase modulator;  
 XX signal transduction tyrosine kinase; tumour; dominant negative mutant;  
 KW cancer; adenocarcinoma; RTK associated disorder; adenocarcinoma;  
 KW angiogenesis; arthritis; diabetic retinopathy; ischaemic heart disease;  
 KW atherosclerosis; inflammation.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.

Key Location/Qualifiers  
 FH Misc-difference 147 /note= "Wild type Lys substituted by Arg"  
 FT  
 FT  
 XX  
 PN WO9964589-A1.  
 PD 16-DEC-1999.  
 XX  
 XX 08-JUN-1999; 99WO-GB001798.  
 PF  
 XX 11-JUN-1998; 98US-0088958P.  
 PR  
 PA (ZONE ) ZENECA LTD.  
 XX  
 PI Ghildyal N, Panchamoorthy G;  
 XX  
 DR WPI; 2000-097538/08.  
 XX  
 XX New nucleic acid encoding human tyrosine kinase, overexpressed in, e.g.  
 PT cancers for treating adenocarcinoma.  
 PT  
 PS Claim 4; Page; 56pp; English.  
 XX  
 CC The present sequence is a dominant negative mutant of human receptor  
 CC tyrosine kinase (RTK), which is obtained by substituting wild type Lys at  
 CC position 147 with Arg. The mutant modulates biological and/or  
 CC pharmacological activity of tyrosine kinase and hence regulates cellular  
 CC and tissue physiology. The present sequence is used for treating many  
 CC diseases related to or mediated by RTK e.g. adenocarcinomas,  
 CC angiogenesis, arthritis, diabetic retinopathy, ischaemic heart disease,  
 CC atherosclerosis, inflammation, solid tumours and metastases. Note: The  
 CC present sequence is not given in the specification but has been derived  
 CC from SEQ ID NO: 3 given in Sequence Listing  
 XX  
 SQ Sequence 422 AA;

Query Match 99.9%; Score 2189; DB 3; Length 422;  
 Best Local Similarity 99.8%; Pred. No. 1.7e-214;  
 Matches 421; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGMTMLLECSLSKLCVIOEKQYEVIVPTLLVTFILLLGVILWLFIREQRTQQORSG 60  
 Db 1 MGMTMLLECSLSKLCVIOEKQYEVIVPTLLVTFILLLGVILWLFIREQRTQQORSG 60  
 QY 61 PQGIAPVPPPRDLSWEAGHGNVALPLKETSVENFLGATTTPALAKLQVPRQLSEVLEQI 120

Db 61 PQGIAPVPPPRDLSWEAGHGNVALPLKETSVENFLGATTTPALAKLQVPRQLSEVLEQI 120  
 QY 121 CSGSCGPIFRANMNTGDPSPKSVILKALKEPAGLHEVQDFLGRIQFHQYLGRKHNVLQ 180  
 Db 121 CSGSCGPIFRANMNTGDPSPKSVILRALKEPAGLHEVQDFLGRIQFHQYLGRKHNVLQ 180  
 QY 181 EGCCTEKLPLYMWLEDAVQAQDILLGFLWTCRRDVTMDGLLYDLTEKQVYHIGKQVLLALE 240  
 Db 181 EGCCTEKLPLYMWLEDAVQAQDILLGFLWTCRRDVTMDGLLYDLTEKQVYHIGKQVLLALE 240  
 QY 241 FLOEKHLFEGDVAARNILMQSDLTAKLCGLIAYEYVTRGAIYSTQTPIKWLAPERLLL 300  
 Db 241 FLOEKHLFEGDVAARNILMQSDLTAKLCGLIAYEYVTRGAIYSTQTPIKWLAPERLLL 300  
 QY 301 RPASIRADVMSFGILLYEMVTLGAPPYEPVPTTSILEHLQRRKIMKRPPSSCTHTMSIMK 360  
 Db 301 RPASIRADVMSFGILLYEMVTLGAPPYEPVPTTSILEHLQRRKIMKRPPSSCTHTMSIMK 360  
 QY 361 SCWRREADRPSPRELRLLEAAIKTADDEAVLQVPELVPELYAAVAGIRVESLFYNYS 420  
 Db 361 SCWRREADRPSPRELRLLEAAIKTADDEAVLQVPELVPELYAAVAGIRVESLFYNYS 420  
 QY 421 ML 422  
 Db 421 ML 422

RESULT 4  
 ID AAU68537 standard; protein; 458 AA.  
 XX AAU68537;  
 XX  
 XX 16-JAN-2002 (first entry)  
 DT Human novel cytokine encoded by cDNA 790CIP2C\_8 #1.  
 DE  
 DE Human; cytokine; cell proliferation; cell differentiation;  
 KW antinflammatory; stem cell growth factor; activin; inhibin; cancer;  
 KW nervous system disease; neuropathy; Alzheimer's disease;  
 KW Parkinson's disease; Huntington's disease; spinal cord disorder;  
 KW head trauma; stroke; myeloid cell disorder; lymphoid cell disorder;  
 KW platelet disorder; thrombocytopaenia; stem cell disorder;  
 KW aplastic anaemia; tissue regeneration; wound healing; ulcer;  
 KW osteoporosis; osteoarthritis; bone degenerative disorder;  
 KW periodontal disease; fibrosis; reperfusion; immune disorder;  
 KW severe combined immunodeficiency; infection; autoimmune disorder;  
 KW multiple sclerosis; rheumatoid arthritis; diabetes mellitus; allergy;  
 KW asthma; coagulation disorder; haemophilia; sepsis; nephritis;  
 KW inflammatory bowel disease; food supplement; immunogen.  
 XX  
 OS Homo sapiens.  
 OS  
 PN WO200175093-A1.  
 XX  
 PD 11-OCT-2001.  
 XX  
 PF 30-MAR-2001; 2001WO-US010484.  
 XX  
 PR 31-MAR-2000; 2000US-00540217.  
 PR 23-AUG-2000; 2000US-00649167.  
 PR 22-SEP-2000; 2000US-00686860.  
 PR 23-OCT-2000; 2000US-00695618.  
 PR 30-NOV-2000; 2000US-00728711.  
 PR 14-MAR-2001; 2001US-00808701.  
 XX  
 PA (HYSE-) HYSEQ INC.  
 XX  
 XX Tang YT, Asundi V, Zhou P, Xue AJ, Ren F, Zhang J, Wang J;  
 PI Xu C, Yang Y, Zaho QA, Chen R, Wang D, Goodrich RW, Liu C;  
 PI Drmanac RT;  
 XX

QY 421 ML 422  
DB 457 ML 458

RESULT 5  
AAG66404  
ID AAG66404 standard; protein; 422 AA.  
XX  
AC AAG66404;  
XX  
DT 17-OCT-2001 (first entry)  
XX  
DE Human fibrous growth factor receptor 46.  
XX  
KW Human; fibrous growth factor receptor 46; cancer; HIV infection;  
XX cytostatic; anti-HIV.  
XX  
OS Homo sapiens.  
XX  
PN CN1296965-A.  
XX  
PD 30-MAY-2001.  
XX  
PF 23-NOV-1999; 99CN-00124072.  
XX  
PR 23-NOV-1999; 99CN-00124072.  
XX  
PA (SHAN-) SHANGHAI BORONG GENE DEV CO LTD.  
XX  
PI Mao Y, Xie Y;  
XX  
DR WPI; 2001-483896/53.  
XX  
N-PSDB; AAH75803.  
XX  
PT Polypeptide-human fibrous growth factor receptor 46 and polynucleotide  
XX for coding said polypeptide.  
XX  
PS Claim 1; Page 22-23 (Disclosure); 29pp; Chinese.  
XX  
CC The present sequence is the protein sequence for human fibrous growth  
XX factor receptor 46. The receptor and its coding sequence are useful in  
XX the treatment of diseases e.g. cancer and HIV infection  
XX  
SQ Sequence 422 AA;

Query Match 99.6%; Score 2183; DB 4; Length 422;  
Best Local Similarity 99.5%; Pred. No. 6.8e-214;  
Matches 420; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MGMTMLLECSLSKLCVIOEQVEVIVPTLLVTFILLLGVILWLFIREQTOOQSG 60  
DB 1 MGMTMLLECSLSKLCVIOEQVEVIVPTLLVTFILLLGVILWLFIREQTOOQSG 60  
QY 61 PQGIAPVPPRDLISWEAGHGNVALPLKETSVENFLGATTAPALAKLOVPREQLSEVLEQI 120  
DB 61 PQGIAPVPPRDLISWEAGHGNVALPLKETSVENFLGATTAPALAKLOVPREQLSEVLEQI 120  
QY 121 CSGSCGPIFRANMTGDPSPKPSVILKALKEPAGLHEVQDFLGRIOFHQYLGKHNVLQ 180  
DB 121 CSGSCGPIFRANMTGDPSPKPSVILKALKEPAGLHEVQDFLGRIOFHQYLGKHNVLQ 180  
QY 181 EGCCTEKLPLYMVLVEDVAQDGLLGLFWTCRRDVTMDGLLYDLTEKQVYHIGKQVLLALE 240  
DB 181 EGCCTEKLPLYMVLVEDVAQDGLLGLFWTCRRDVTMDGLLYDLTEKQVYHIGKQVLLALE 240  
QY 241 FLOEKHLFGHDVAARNILMQSDLTAKLCGLGLAYEVYTRGAISSQTPIPLKWLAPERLLL 300  
DB 241 FLOEKHLFGHDVAARNILMQSDLTAKLCGLGLAYEVYTRGAISSQTPIPLKWLAPERLLL 300  
QY 301 RPASIRADVWSFGILLYEMVTLGAPPYVEPPTTSILEHLQRRKMKRPSSCTHTMYSTMK 360  
DB 301 RPASIRADVWSFGILLYEMVTLGAPPYVEPPTTSILEHLQRRKMKRPSSCTHTMYSTMK 360

DR WPI; 2001-626432/72.  
DR N-PSDB; AAS59829.  
XX  
XX New polypeptides and nucleic acids, useful for diagnosis, treatment of  
XX inflammatory, autoimmune, neurological, myeloid or lymphoid cell, bone  
XX degenerative disorders, cancer and promoting wound healing.  
PS Claim 20; Page 261; 336pp; English.

The invention relates to isolated human polypeptides (which may be  
cytokines) and the polynucleotides encoding them. The protein is useful  
for identifying a compound which binds to it (e.g. modulators, agonists  
and antagonists). The polynucleotides are useful as an array for mismatch  
detection. The proteins and nucleic acids are useful as nutritional  
sources or supplements. The protein exhibits exhibits activity relating  
to cytokine, cell proliferation, cell differentiation, antiinflammatory,  
stem cell growth factor activity, immune stimulating or immune  
suppressing and activin or inhibin related activities. The proteins (and  
antibodies raised against them) and nucleic acids are therefore useful in  
the diagnosis and treatment of diseases and disorders such as cancer,  
central and peripheral nervous system diseases and neuropathies,  
Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic  
lateral sclerosis, spinal cord disorders, head trauma, cerebrovascular  
diseases, stroke, myeloid or lymphoid cell disorders, platelet disorders,  
thrombocytopaenia, stem cell disorders, aplastic anaemia, for  
regeneration of bone, cartilage, tendon, ligament and/or nerve tissue  
growth, and in tissue repair, healing of burns, incisions, ulcers, or  
treating osteoporosis, osteoarthritis, bone degenerative disorders, or  
periodontal disease, lung or liver fibrosis, reperfusion injury in  
various tissues, various immune deficiencies and disorders including  
severe combined immunodeficiency (SCID), bacterial or fungal infections,  
autoimmune disorders (e.g. multiple sclerosis, rheumatoid arthritis,  
diabetes mellitus, myasthenia gravis), allergic reactions and conditions,  
such as asthma or other respiratory problems, coagulation disorders,  
haemophilia), septic shock, sepsis, arthritis, nephritis and inflammatory  
bowel disease, viral infection and are useful in altering bodily  
characteristics. The present sequence represents a novel protein of the  
invention

XX  
SQ Sequence 458 AA;

Query Match 99.8%; Score 2186; DB 4; Length 458;  
Best Local Similarity 99.8%; Pred. No. 2.4e-214;  
Matches 421; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGMTMLLECSLSKLCVIOEQVEVIVPTLLVTFILLLGVILWLFIREQTOOQSG 60  
DB 37 MGMTMLLECSLSKLCVIOEQVEVIVPTLLVTFILLLGVILWLFIREQTOOQSG 96  
QY 61 PQGIAPVPPRDLISWEAGHGNVALPLKETSVENFLGATTAPALAKLOVPREQLSEVLEQI 120  
DB 97 PQGIAPVPPRDLISWEAGHGNVALPLKETSVENFLGATTAPALAKLOVPREQLSEVLEQI 156  
QY 121 CSGSCGPIFRANMTGDPSPKPSVILKALKEPAGLHEVQDFLGRIOFHQYLGKHNVLQ 180  
DB 157 CSGSCGPIFRANMTGDPSPKPSVILKALKEPAGLHEVQDFLGRIOFHQYLGKHNVLQ 216  
QY 181 EGCCTEKLPLYMVLVEDVAQDGLLGLFWTCRRDVTMDGLLYDLTEKQVYHIGKQVLLALE 240  
DB 217 EGCCTEKLPLYMVLVEDVAQDGLLGLFWTCRRDVTMDGLLYDLTEKQVYHIGKQVLLALE 276  
QY 241 FLOEKHLFGHDVAARNILMQSDLTAKLCGLGLAYEVYTRGAISSQTPIPLKWLAPERLLL 300  
DB 277 FLOEKHLFGHDVAARNILMQSDLTAKLCGLGLAYEVYTRGAISSQTPIPLKWLAPERLLL 336  
QY 301 RPASIRADVWSFGILLYEMVTLGAPPYVEPPTTSILEHLQRRKMKRPSSCTHTMYSTMK 360  
DB 337 RPASIRADVWSFGILLYEMVTLGAPPYVEPPTTSILEHLQRRKMKRPSSCTHTMYSTMK 396  
QY 361 SCWRREADRSPRELRLRLAAIKTADDEAVLQVPELVVPELVYAAGIRVESLFYNS 420  
DB 397 SCWRREADRSPRELRLRLAAIKTADDEAVLQVPELVVPELVYAAGIRVESLFYNS 456

QY 361 SCWRREADRPSRELRLRLAAIKTADDEAVLQVPELVVPELYAAVAGIRVESLFYNYS 420  
 DB 361 SCWRREADRPSRELRLRLAAIKTADDEAVLQVPELVVPELYAAVAGIRVESLFYNYS 420  
 QY 421 ML 422  
 DB 421 ML 422

RESULT 6  
 AAY44298  
 ID AAY44298 standard; protein; 421 AA.  
 XX  
 AC AAY44298;  
 DT 29-FEB-2000 (first entry)  
 XX  
 DE Human receptor tyrosine kinase dominant negative mutant-1.  
 XX  
 KW Human; receptor tyrosine kinase; RTK; tyrosine kinase modulator;  
 KW signal transduction tyrosine kinase; tumour; dominant negative mutant;  
 KW cancer; adenocarcinoma; RTK associated disorder; adenocarcinoma;  
 KW angiogenesis; arthritis; diabetic retinopathy; ischaemic heart disease;  
 KW atherosclerosis; inflammation.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.

Key Location/Qualifiers  
 FT Misc-difference 146..147  
 FT /note= "Wild type Lys at position 147 is deleted"  
 XX  
 PN WO9964589-A1.  
 PD 16-DEC-1999.  
 XX  
 PF 08-JUN-1999; 99WO-GB001798.  
 XX  
 PR 11-JUN-1998; 98US-00889598.  
 PA (ZENE ) ZENECA LTD.  
 XX  
 PI Ghildyal N, Panchamoorthy G;  
 XX  
 DR WPI; 2000-097538/08.  
 XX  
 PT New nucleic acid encoding human tyrosine kinase, overexpressed in, e.g.  
 PT cancers for treating adenocarcinoma.  
 XX  
 PS Claim 3; Page; 56pp; English.  
 CC  
 CC The present sequence is a dominant negative mutant of human receptor  
 CC tyrosine kinase (RTK), which is obtained by deleting Lys at position 147  
 CC of wild type sequence. The mutant modulates biological and/or  
 CC pharmacological activity of tyrosine kinase and hence regulates cellular  
 CC and tissue physiology. The present sequence is used for treating many  
 CC diseases related to or mediated by RTK e.g. adenocarcinomas,  
 CC angiogenesis, arthritis, diabetic retinopathy, ischaemic heart disease,  
 CC atherosclerosis, inflammation, solid tumours and metastases. Note: The  
 CC present sequence is not given in the specification but has been derived  
 CC from SEQ ID NO: 3 given in Sequence Listing  
 XX  
 SQ Sequence 421 AA;

Query Match 99.3%; Score 2176.5; DB 3; Length 421;  
 Best Local Similarity 99.8%; Pred. No. 3.1e-213;  
 Matches 421; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 MGWTRMLECSLSKLCVIOQKEVLIIVPTLLVTFILILGVILWLFIREQRTQQQRSG 60  
 DB 1 MGWTRMLECSLSKLCVIOQKEVLIIVPTLLVTFILILGVILWLFIREQRTQQQRSG 60

QY 61 PQGIAPVPPRDLUSWEAGHGNVALPLKETSVENFLGATTPALAKLOVPPREQLSEVLEQI 120  
 DB 61 PQGIAPVPPRDLUSWEAGHGNVALPLKETSVENFLGATTPALAKLOVPPREQLSEVLEQI 120  
 QY 121 CSGSCGPIFRANNMTGDPSPKSVILKALKEPAGLHEVQDFLGRIOPHOYLGHKHNVLQ 180  
 DB 121 CSGSCGPIFRANNMTGDPSPKSVIL-ALKEPAGLHEVQDFLGRIOPHOYLGHKHNVLQ 179  
 QY 181 EGCCTEKLPLYMVLEDAQDGLLGLFWLTCRRDVTMDGLLYDLTERQVYHGHQVLLALE 240  
 DB 180 EGCCTEKLPLYMVLEDAQDGLLGLFWLTCRRDVTMDGLLYDLTERQVYHGHQVLLALE 239  
 QY 241 FLQEKHLFHGDVAARNILMQSDLTAKLCGLGLAYEYVTRGAISSTOTIPKMLAPERLLL 300  
 DB 240 FLQEKHLFHGDVAARNILMQSDLTAKLCGLGLAYEYVTRGAISSTOTIPKMLAPERLLL 299  
 QY 301 RPASIRADVWSFGILLYEMVTLGAPPYPEVPPTSILHLQRRKIMKRPSSCTHTWYSIMK 360  
 DB 300 RPASIRADVWSFGILLYEMVTLGAPPYPEVPPTSILHLQRRKIMKRPSSCTHTWYSIMK 359  
 QY 361 SCWRREADRPSRELRLRLAAIKTADDEAVLQVPELVVPELYAAVAGIRVESLFYNYS 420  
 DB 360 SCWRREADRPSRELRLRLAAIKTADDEAVLQVPELVVPELYAAVAGIRVESLFYNYS 419  
 QY 421 ML 422  
 DB 420 ML 421

RESULT 7  
 AAB66603  
 ID AAB66603 standard; protein; 209 AA.  
 XX  
 AC AAB66603;  
 DT 04-APR-2001 (first entry)  
 XX  
 DE Human h14833 protein.  
 XX  
 KW Human; protein kinase; cell growth; tumour; cancer; immune; inflammatory;  
 KW respiratory; haematological; bone disorder.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200100879-A1.  
 XX  
 PD 04-JAN-2001.  
 XX  
 PF 30-JUN-2000; 2000WO-US018291.  
 XX  
 PR 30-JUN-1999; 99US-00345473.  
 PR 01-MAY-2000; 2000US-00562480.  
 XX  
 PA (MILL-) MILLENNIUM PHARM INC.  
 PI Hodge MR, Meyers R, Williamson M;  
 XX  
 DR WPI; 2001-061977/07.  
 XX  
 PT New protein kinase polypeptides, nucleic acids and anti-kinase  
 PT antibodies, useful for diagnosing and treating e.g. cancer, inflammatory,  
 PT immune, cardiovascular and bone disorders.  
 XX  
 PS Claim 1; Fig 7; 93pp; English.  
 XX  
 CC The present invention relates to human protein kinase. The proteins are  
 CC from new human genes termed h12832, h14138, h14833, h15990, h15993,  
 CC h16341 and h2252. The proteins may be used to identify modulators of  
 CC their activity. The proteins may also be used to derive products for the  
 CC treatment of cellular growth related disorders, malignancies, cancers,  
 CC immune, inflammatory, respiratory, haematological and bone-related  
 CC disorders  
 XX

SQ Sequence 209 AA;  
Query Match 49.2%; Score 1079; DB 4; Length 209;  
Best Local Similarity 100.0%; Pred. No. 1.7e-101;  
Matches 209; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 214 MTMDGLLYDLTEKQVYHIGKQVLLALEFLQEKHLPHGDAARNILMQSDLTAKLCGLGLA 273  
DB 1 MTMDGLLYDLTEKQVYHIGKQVLLALEFLQEKHLPHGDAARNILMQSDLTAKLCGLGLA 60  
QY 274 YEVYTRGAISSQTITPLKWLAPERLLLRPASIRADVWVSGILLYEMVTLGAPPYEPVPT 333  
DB 61 YEVYTRGAISSQTITPLKWLAPERLLLRPASIRADVWVSGILLYEMVTLGAPPYEPVPT 120  
QY 334 STLEHLQRRKIMKRPSSCTHTMYSMKSCWRREADRSPRELRLRLAEAAIKTADDEAVL 393  
DB 121 STLEHLQRRKIMKRPSSCTHTMYSMKSCWRREADRSPRELRLRLAEAAIKTADDEAVL 180  
QY 394 QVPELVVPELYAAVAGIRVESLFYNYSM 422  
DB 181 QVPELVVPELYAAVAGIRVESLFYNYSM 209  
RESULT 8  
ID AAB65707 standard; protein; 183 AA.  
XX AAB65707;  
XX 27-MAR-2001 (first entry)  
DE Novel protein kinase, SEQ ID NO: 236.  
XX Human; mouse; protein kinase; antiarthritic; antisclerotic; osteopathic;  
KW immunosuppressive; cardiac; renal; antiinflammatory; antiasthmatic;  
KW dermatological; antidiabetic; antifertility; gene therapy; vaccine;  
KW immune disorder; cardiovascular disease; neurodegenerative disease;  
KW cancer; autoimmune disorder; stroke; inflammatory bowel disease;  
KW inflammatory pelvic disease; multiple sclerosis; psoriasis.  
XX Mus musculus.  
XX WO200073469-A2.  
XX 07-DEC-2000.  
XX 26-MAY-2000; 2000WO-US014842.  
XX 28-MAY-1999; 99US-0136503P.  
XX (SUGEN-) SUGEN INC.  
XX Plowman GD, Martinez R, Whyte D, Sudersanam S;  
XX WPI; 2001-032161/04.  
XX N-PSDB; AAF44736.  
XX Nucleic acids encoding kinase polypeptides, useful for diagnosing and  
PT treating immune-related diseases and disorders, cardiovascular disease,  
PT neurodegenerative diseases and/or cancers.  
XX Claim 10; Fig 1; 310pp; English.  
XX The present sequence is a novel protein kinase. The novel protein kinases  
CC and the nucleic acids that encode them may be used in the treatment and  
CC diagnosis of diseases associated with inappropriate kinase expression  
CC such as immune-related diseases and disorders, cardiovascular disease,  
CC neurodegenerative diseases and/or cancers. The nucleic acids and  
CC complementary sequences may also be used as DNA probes in diagnostic  
CC assays. The kinase polypeptides may be used as antigens in the production  
CC of antibodies of kinase expression and activity. Anti-kinase antibodies  
CC and kinase antagonists may also be used to down regulate kinase  
CC expression and activity. Diseases related to kinase expression and

CC activity include rheumatoid arthritis, atherosclerosis, autoimmune  
CC disorders, complications of organ transplantation, myocardial infarction,  
CC immune disorders, cardiomyopathies, strokes, renal failure, oxidative-  
CC stress related disorders, chronic inflammatory bowel disease, chronic  
CC inflammatory pelvic disease, multiple sclerosis, asthma, osteoarthritis,  
CC psoriasis, rhinitis, autoimmunity, diabetes, cancers and reproductive  
CC disorders  
SQ Sequence 183 AA;  
Query Match 33.9%; Score 743; DB 4; Length 183;  
Best Local Similarity 78.7%; Pred. No. 3.1e-67;  
Matches 144; Conservative 17; Mismatches 20; Indels 2; Gaps 1;  
QY 242 LOEKHLFGDVAARNILMQSDLTAKLCGLGLAYEYVYTRGAISS--TOTIPLKWLAPERLL 299  
DB 1 LOEKHLFGDVAARNILMQSDLTAKLCGLGLAYEYVYTRGAISS--TOTIPLKWLAPERLL 60  
QY 300 LRPASIRADVWVSGILLYEMVTLGAPPYEPVPTSIHLQRRKIMKRPSSCTHTMYSTM 359  
DB 61 LRPASIRADVWVSGILLYEMVTLGAPPYEPVPTSIHLQRRKIMKRPSSCTHTMYSTM 120  
QY 360 KSCWRREADRSPRELRLRLAEAAIKTADDEAVLQVPELVVPELYAAVAGIRVESLFYNY 419  
DB 121 KSCWRREADRSPRELRLRLAEAAIKTADDEAVLQVPELVVPELYAAVAGIRVESLFYNY 180  
QY 420 SML 422  
DB 181 SVL 183  
RESULT 9  
ID AAE00672 standard; protein; 104 AA.  
XX AAE00672;  
XX 02-JUL-2001 (first entry)  
XX Human protein tyrosine kinase receptor (PTK) from clone HAGHE04.  
XX Human; protein tyrosine kinase receptor; PTK; antibacterial; antiviral;  
KW antifungal; antiparasitic; sarcoidosis; inflammation; asthma; arthritis;  
KW cardiovascular disorder; severe combined immunodeficiency; SCID; vaccine;  
KW hyperproliferative disorder; atherosclerosis; brain disorder; leukaemia;  
KW multiple sclerosis; Alzheimer's disease; vascular dementia; thrombosis;  
KW neurodegenerative disorder; gastrointestinal disorder; cancer; lymphoma;  
KW blood coagulation disorder; trauma; cerebrovascular disorder; tendonitis;  
KW gene therapy; nephrotic syndrome; glomerulonephritis; allergy; neoplasm;  
KW musculo-skeletal disorder; Parkinson's disease; autoimmune disorder;  
KW behavioural disorder; renal disorder.  
XX Homo sapiens.  
XX Key Location/Qualifiers  
XX Region 8..13 /label= Immunogenic\_epitope  
XX Region 22..33 /label= Immunogenic\_epitope  
XX Region 43..57 /label= Immunogenic\_epitope  
XX WO200129564-A1.  
XX 26-APR-2001.  
XX 12-OCT-2000; 2000WO-US028066.  
XX 15-OCT-1999; 99US-0159542P.  
XX 17-NOV-1999; 99US-0165914P.  
XX 14-MAR-2000; 2000US-0189027P.  
XX (HUMA-) HUMAN GENOME SCI INC.  
XX

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XX Ruben SM, Shi Y, Young PE, Ni J;
PI WPI; 2001-290976/30.
XX N-PSDB; AAD03998.
DR New isolated nucleic acid molecule for producing human protein tyrosine
PT kinase receptor.
XX Claim 12; Page 283; 288pp; English.
XX The present sequence is human protein tyrosine kinase receptor (PTK) from
CC clone HAGHE04. The invention relates to human protein tyrosine kinase
CC (PTK) receptors and their corresponding cDNA molecules. PTK receptors are
CC useful in providing immunological probes for differential identification
CC of the tissues or cell types present in a biological sample. PTK is used
CC in methods for the diagnosis, prevention and treatment of various
CC disorders related to PTK such as immune system disorders (severe combined
CC immunodeficiency (SCID), inflammation); hyperproliferative disorders
CC (neoplasia, sarcoidosis); cardiovascular disorders (arrhythmia,
CC atherosclerosis); central nervous system disorders (multiple sclerosis),
CC neurodegenerative disorders (Alzheimer's disease, Parkinson's disease);
CC blood coagulation disorders (thrombocytopaenia); autoimmune disorders
CC (biliary cirrhosis, Crohn's disease); respiratory disorders (asthma,
CC allergy); gastrointestinal disorders (inflammatory bowel disease);
CC cerebrovascular disorders (thrombosis, vascular dementia); brain
CC disorders (phenylketonuria); cancers (such as ovarian, lung, bladder,
CC liver, breast and lymphomas); behavioural disorders (Tourette's syndrome)
CC ; musculo-skeletal disorders (arthritis, trauma, tendonitis); renal
CC disorders (nephrotic syndrome, glomerulonephritis); metastases of
CC malignancies and related disorders (leukaemia, multiple myeloma); and
CC infections caused by bacteria, viruses, fungi and parasites. PTK is also
CC useful for screening therapeutic compounds. PTK is used as an antigen in
CC a vaccine to raise an immune response against infectious disease. PTK
CC nucleic acids are useful in gene therapy
XX Sequence 104 AA;
XX
XX Query Match 24.7%; Score 542; DB 4; Length 104;
XX Best Local Similarity 100.0%; Pred. No. 4.8e-47;
XX Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 319 MVTLGAPPYPEVPTTSILEHLQRRKIMKRPSSCTHTMTYIMKSCWRWEADRPSPRELR 378
XX Db 1 MVTLGAPPYPEVPTTSILEHLQRRKIMKRPSSCTHTMTYIMKSCWRWEADRPSPRELR 60
XX
XX QY 379 RLEAAIKTADDEAVLQVPELVPELYAAVAGIRVESLFYNSML 422
XX Db 61 RLEAAIKTADDEAVLQVPELVPELYAAVAGIRVESLFYNSML 104
XX
XX RESULT 10
XX ABB43239
XX ID ABB43239 standard; peptide; 93 AA.
XX AC ABB43239;
XX DT 04-FEB-2002 (first entry)
XX DE Peptide #10745 encoded by human foetal liver single exon probe.
XX KW Human; foetal liver; gene expression; single exon nucleic acid probe.
XX OS Homo sapiens.
XX FN WO200157277-A2.
XX XX
XX PD 09-AUG-2001.
XX PF 30-JAN-2001; 2001WO-US0000669.
XX XX
XX QY 04-FEB-2000; 2000US-0180312P.
XX PR 26-MAY-2000; 2000US-0207456P.
XX
XX Ruben SG, Hanzel DK, Chen W, Rank DR;
PI WPI; 2001-483447/52.
XX Human genome-derived single exon nucleic acid probes useful for analyzing
CC gene expression in human foetal liver.
XX Claim 27; SEQ ID NO 35874; 639pp + Sequence Listing; English.
XX The invention relates to a single exon nucleic acid probe for measuring
CC human gene expression in a sample derived from human foetal liver. The
CC single exon nucleic acid probes may be used for predicting, measuring and
CC displaying gene expression in samples derived from human foetal liver. The
CC present sequence is a peptide encoded by a single exon nucleic acid probe
CC of the invention. Note: The sequence data for this patent did not form
CC part of the printed specification, but was obtained in electronic format
CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX Sequence 93 AA;
XX
XX Query Match 20.6%; Score 452; DB 4; Length 93;
XX Best Local Similarity 100.0%; Pred. No. 6.4e-38;
XX Matches 87; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 64 IAPVPPPPDLGWEAGHGNNVALPLKETSVENFLGATTALAKLQVPREQLSEVLQICSG 123
XX Db 1 IAPVPPPPDLGWEAGHGNNVALPLKETSVENFLGATTALAKLQVPREQLSEVLQICSG 50
XX
XX QY 124 SCGPFRFRAMNTGDPSPKPSVILKALK 150
XX Db 61 SCGPFRFRAMNTGDPSPKPSVILKALK 87
XX
XX RESULT 11
XX AAM37079
XX ID AAM37079 standard; protein; 93 AA.
XX AC AAM37079;
XX DT 17-OCT-2001 (first entry)
XX DE Peptide #11116 encoded by probe for measuring placental gene expression.
XX KW Probe; microarray; human; placenta; antenatal diagnosis;
XX genetic disorder.
XX OS Homo sapiens.
XX FN WO200157272-A2.
XX XX
XX PD 09-AUG-2001.
XX PF 30-JAN-2001; 2001WO-US0000663.
XX XX
XX QY 04-FEB-2000; 2000US-0180312P.
XX PR 26-MAY-2000; 2000US-0207456P.
XX 30-JUN-2000; 2000US-00608408.
XX 03-AUG-2000; 2000US-00632366.
XX 21-SEP-2000; 2000US-0234587P.
XX 27-SEP-2000; 2000US-0236359P.
XX 04-OCT-2000; 2000GB-00024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX Penn SG, Hanzel DK, Chen W, Rank DR;
PI

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XX DR WPI; 2001-48897/53.  
 XX PT Human genome-derived single exon nucleic acid probes useful for analyzing  
 XX PT gene expression in human placenta.  
 XX PS Claim 27; SEQ ID NO 37348; 654pp; English.  
 XX CC The present invention relates to single exon nucleic acid probes (SENP;  
 CC see AA131315-AA157546). The present sequence is a peptide encoded by one  
 CC such probe. The probes are useful for producing a microarray for  
 CC predicting, measuring and displaying gene expression in samples derived  
 CC from human placenta. The probes are useful for antenatal diagnosis of  
 CC human genetic disorders  
 XX SQ Sequence 93 AA;  
 Query Match 20.6%; Score 452; DB 4; Length 93;  
 Best Local Similarity 100.0%; Pred. No. 6.4e-38;  
 Matches 87; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 64 IAPVPPRDLSEAGHGNNVALPLKETSVENFLGATTTPALAKIQVPREQLSEVLEICSG 123  
 Db 1 IAPVPPRDLSEAGHGNNVALPLKETSVENFLGATTTPALAKIQVPREQLSEVLEICSG 60  
 QY 124 SCGPFRANNTGDPSPKPKSVILKALK 150  
 Db 61 SCGPFRANNTGDPSPKPKSVILKALK 87  
 RESULT 12  
 AAM76972  
 ID AAM76972 standard; protein; 93 AA.  
 AC AAM76972;  
 XX 06-NOV-2001 (first entry)  
 XX Human bone marrow expressed probe encoded protein SEQ ID NO: 37278.  
 XX Human; bone marrow expressed exon; gene expression analysis; probe;  
 KW microarray; cancer; leukaemia; lymphoma; myeloma.  
 XX Homo sapiens.  
 OS WO200157276-A2.  
 XX 09-AUG-2001.  
 XX 30-JAN-2001; 2001WO-US000668.  
 XX 04-FEB-2000; 2000US-0180312P.  
 XX 26-MAY-2000; 2000US-0207456P.  
 XX 30-JUN-2000; 2000US-00608408.  
 XX 03-AUG-2000; 2000US-00632366.  
 XX 21-SEP-2000; 2000US-0234687P.  
 XX 27-SEP-2000; 2000US-0236359P.  
 XX 04-OCT-2000; 2000GB-00024263.  
 (MOLE-) MOLECULAR DYNAMICS INC.  
 XX Penn SG, Hanzel DK, Chen W, Rank DR;  
 XX WPI; 2001-488900/53.  
 XX Human genome-derived single exon nucleic acid probes useful for analyzing  
 XX gene expression in human bone marrow.  
 XX Example 4; SEQ ID NO 37278; 658pp + Sequence Listing; English.  
 XX The present invention provides a number of single exon nucleic acid  
 CC probes which are derived from genomic sequences expressed in the human  
 CC bone marrow. They can be used to measure gene expression in bone marrow

CC samples, which may enable the improved diagnosis and treatment of cancers  
 CC such as lymphoma, leukaemia and myeloma. The present sequence is a  
 CC protein encoded by one of the probes of the invention  
 XX SQ Sequence 93 AA;  
 Query Match 20.6%; Score 452; DB 4; Length 93;  
 Best Local Similarity 100.0%; Pred. No. 6.4e-38;  
 Matches 87; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 64 IAPVPPRDLSEAGHGNNVALPLKETSVENFLGATTTPALAKIQVPREQLSEVLEICSG 123  
 Db 1 IAPVPPRDLSEAGHGNNVALPLKETSVENFLGATTTPALAKIQVPREQLSEVLEICSG 60  
 QY 124 SCGPFRANNTGDPSPKPKSVILKALK 150  
 Db 61 SCGPFRANNTGDPSPKPKSVILKALK 87  
 RESULT 13  
 AAM64146  
 ID AAM64146 standard; protein; 93 AA.  
 AC AAM64146;  
 XX 05-NOV-2001 (first entry)  
 XX Human brain expressed single exon probe encoded protein SEQ ID NO: 36251.  
 XX Human; brain expressed exon; gene expression analysis; probe; microarray;  
 KW Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer.  
 XX Homo sapiens.  
 OS WO200157275-A2.  
 XX 09-AUG-2001.  
 XX 30-JAN-2001; 2001WO-US000667.  
 XX 04-FEB-2000; 2000US-0180312P.  
 XX 26-MAY-2000; 2000US-0207456P.  
 XX 30-JUN-2000; 2000US-00608408.  
 XX 03-AUG-2000; 2000US-00632366.  
 XX 21-SEP-2000; 2000US-0234687P.  
 XX 27-SEP-2000; 2000US-0236359P.  
 XX 04-OCT-2000; 2000GB-00024263.  
 (MOLE-) MOLECULAR DYNAMICS INC.  
 XX Penn SG, Hanzel DK, Chen W, Rank DR;  
 XX WPI; 2001-483446/52.  
 XX Single exon nucleic acid probes for analyzing gene expression in human  
 XX brains.  
 XX Example 4; SEQ ID NO 36251; 650pp + Sequence Listing; English.  
 XX The present invention provides a number of single exon nucleic acid  
 CC probes which are derived from genomic sequences expressed in the human  
 CC brain. They can be used to measure gene expression in brain cell samples,  
 CC which may enable the diagnosis and improved treatment of nervous system  
 CC diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,  
 CC epilepsy and cancers. The present sequence is a protein encoded by one of  
 CC the probes of the invention  
 XX SQ Sequence 93 AA;  
 Query Match 20.6%; Score 452; DB 4; Length 93;  
 Best Local Similarity 100.0%; Pred. No. 6.4e-38;  
 Matches 87; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	64	IAPVPPRDLSEAGHGGNVALPLKETS	VENFLGATTAPALAKLQVPREQL	CSG 123
Db	1	IAPVPPRDLSEAGHGGNVALPLKETS	VENFLGATTAPALAKLQVPREQL	CSG 60
Qy	124	SCGPIFRANMNTGDPSPKSVILKALK	150	
Db	61	SCGPIFRANMNTGDPSPKSVILKALK	87	

RESULT 14  
ABG58633  
ID ABG58633 standard; peptide; 93 AA.  
XX  
AC ABG58633:

DT 25-FEB-2003 (first entry)

Human liver peptide, SEQ ID No 37281.

KW Human; liver; cirrhosis; hyperlipoproteinaemia; hyperlipidaemia;  
KW hypercholesterolaemia; coronary heart disease.  
5247

OS Homo sapiens.

AA  
PN  
WO200157273-A2.

XX  
PD 09-AUG-2001.

XX  
PF  
30-JAN-2001; 2001WO-US000664.

PR 04-FEB-2000; 2000US-0180312P.

26-MAY-2000; 2000US-0207456P.  
30-JUN-2000; 2000US-00608408.

PR 03-AUG-2000; 2000US-00632366.  
PR 21-SEP-2000; 2000US-0234687D

27-SEP-2000; 2000US-0236359P.  
04-OCT-2000: 2000GB-00021263

XX  
PA  
(MOLE-) MOLECULAR DYNAMICS INC.

Penn SG, Hanzel DK, Chen W, Rank DR;

WPI; 2001-488898/53.

Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human adult liver.

Claim 27; SEQ ID NO 37281; 658pp; English.

The invention relates to a single exon nucleic acid probe (SENP) (I) for measuring human gene expression in a sample derived from human adult liver, comprising one of 13109 defined nucleotide sequences given in the specification (or complements/ fragments). The probe hybridises at high stringency to a nucleic acid molecule expressed in the human adult liver. (I) may be used for predicting, measuring and displaying gene expression in samples derived from human adult liver. The genes identified may be involved in genetic liver diseases such as cirrhosis, hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which is associated with coronary heart disease. ABG47348-ABG59930 represent human liver single exon encoded peptides of the invention. Note: The sequence information for this patent does not appear in the printed specification but was obtained in electronic format directly from WIPO at [ftp.wipo.int/pub/published/pct/sequences](http://wipo.int/pub/published/pct/sequences)

Sequence 93 AA;

Query Match	20.6%;	Score 452;	DB 4;	Length 93;
Best Local Similarity	100.0%;	Pred. No. 6.4e-38;		
Matched	07			

64 IAPVPPRDLSEAGHGNNVALPKETSVENFLGATTPALAKVQPREQLSEVLQICSG 123  
1 IAPVPPRDLSEAGHGNNVALPKETSVENFLGATTPALAKVQPREQLSEVLQICSG 60

Qy	124	SCGPIFRANMNTGDPSPKPSVILKALK	150
Db	61	SCGPIFRANMNTGDPSPKPSVILKALK	87

RESULT 15

AAE21977  
ID AAE21977 standard; protein; 801 AA.

AC AAE21977;

AA  
DT 16-JUL-2002 (first entry)

Mouse fibroblast growth factor receptor 3 (FGFR3) mutant protein.

KW Mouse; chondrodysplasia; achondroplasia; transgenic mouse; therapy;  
KW fibroblast growth factor receptor 3; FGFR3; limb; midface hypoplasia;  
KW large skull; drug screening; drug development; transgenic; mutant;  
KW mutin.

XX  
OS  
Mus sp.

OS Synthetic.

XX  
PN  
US6265632-B1.XX  
PD 24-JUL-2001.XX  
PF 26-AUG-1999.XX  
PR 27-AUG-1998.XX  
PA (VEDA ) VEDAPA (PROC-) PROC  
XX

Yayon A, Segev O;

DR WPI; 2001-463946/50.

XX  
DE

transgenic mice having a genetically modified fibroblast growth factor receptor gene, useful as a model for human chondrodysplasia, e.g. achondroplasia characterized by shortening of the limbs, midface hypoplasia or large skull.

Example: Col 65-70; 49pp; English.

The invention relates to an animal model for chondrodysplasia, more particularly, to a transgenic mouse model for achondroplasia. This transgenic mouse contains a fibroblast growth factor receptor 3 (FGFR3) gene including a G to A point mutation changing Gly to Arg in codon 380 in its genome. The transgenic mouse is useful as a model for FGFR3 associated chondrodysplasia, particularly FGFR3 achondroplasia, e.g., shortening of the limbs, midface hypoplasia and large skull. This model can be exploited to gain better understanding of the disease and as an experimental model with which experimental therapy to chondrodysplasias can be exercised. The transgenic mouse is particularly useful as a tool for screening, developing and evaluating drugs with a potential of relieving or abolishing chondrodysplasia syndromes and/or symptoms. The present sequence is mouse FGFR3 mutant protein

Q Sequence 801 AA;

Query Match	20.3%;	Score 444;	DB 4;	Length 801;
Best Local Similarity	30.5%;	Pred. No. 1e-35;		

34 VTIFLILGLVILWLFIRQRTQQRSRGGIAPV---PPRDLSWEACHGNNVALPKET 90  
| | | : | : | : | : | : | : | : | : | : | : | : | : | : |  
375 VVFELFILWAARVILCLRSLRPKKGSGPTVHKYSRFLFKRKQSVLESNNSNTPL--V 432

91 SVENFLGATTPALA---KLQVP-----REQLSEVLEQICSGSCGPIFRANNTGD 137

Tue Jun 15 09:35:26 2004

Db 433 RIARLSGEGPVLANVSELELPADPKWELSTRITLKGPIGEGCGVVMAEIGIDKDR 492  
QY 138 PSKPKSVILKALKEPAGLHEVQDFLGRIOFHQYLGKHKHNLVQLEGCCTEKLPYMWLEDV 197  
Db 493 TAKPVTVAVKMLKODATDKDLSDLVSEMEMMKMIGKHKNIINLLGACTGGGPLYVLVEYA 552  
QY 198 AQGDILGFLWTCRRDVTMDGLLY-----DLTEKQVYHIGKOVLLALEFLQEKHL 247  
Db 553 AKGNLREEL-RARRP---PGMDYSFDACRLPEEQLTCKDLVSCAYQVARGMEYLASOKC 607  
QY 248 PHGDVAARNILMQSDLTAKLGLGLAYEVYTRGAISSTQT--IPLKWLAPERLLLRPAS 305  
Db 608 THRDGAARNVLVTEDNVWKIADFGGLARDVHNLDDYKKTNGELPVKMWAPALFDRVYTH 667  
QY 306 RADVWSFGILLYEMVTLGAP-PYPEVPPTSILEHLQRRKIMKRPPSCTHTMYSIMKSCWR 364  
Db 668 QSDVWSFGVLLWEIFTPGGFSPVPGIPVEBELFKLLKEGHRMDKPAASCTHDLYMIMRECWH 727  
QY 365 WREARPPSPRELRLLE--AAIKTADDEAVLOVP 396  
Db 728 AVESQRPTEKQLVEDLDRILTITVTSTDEYLDLSVP 761

Search completed: June 14, 2004, 18:44:17  
Job time : 61 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 14, 2004, 18:41:39 ; Search time 45 seconds  
(without alignments)  
2958.860 Million cell updates/sec

Title: US-10-040-884-3  
Perfect score: 2192  
Sequence: 1 MGMTMLLECSLSKLCVQ.....LYAAVAGIRVESLFYNYSML 422

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SPTREMBL 25:\*

- 1: sp\_archea:\*
- 2: sp\_bacteria:\*
- 3: sp\_fungi:\*
- 4: sp\_human:\*
- 5: sp\_invertebrate:\*
- 6: sp\_mammal:\*
- 7: sp\_mhc:\*
- 8: sp\_organelle:\*
- 9: sp\_phage:\*
- 10: sp\_plant:\*
- 11: sp\_rodent:\*
- 12: sp\_virus:\*
- 13: sp\_vertebrate:\*
- 14: sp\_unclassified:\*
- 15: sp\_rvirus:\*
- 16: sp\_bacteriap:\*
- 17: sp\_archeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	2192	100.0	422	4	Q9NSH1	Q9ns11 homo sapien
2	2183	99.6	422	4	Q9BXY2	Q9bxy2 homo sapien
3	1684.5	76.8	429	11	Q8BZT1	Q8bzt1 mus musculus
4	1357	61.9	340	11	Q8BZH6	Q8bzh6 mus musculus
5	467.5	21.3	828	13	Q9DGK3	Q9dgg3 xenopus lae
6	467.5	21.3	829	13	Q9PSV8	Q9psv8 xenopus lae
7	464.5	21.2	800	13	Q918X3	Q918x3 brachydanio
8	461	21.0	828	13	Q91743	Q91743 xenopus lae
9	459.5	21.0	818	13	Q91742	Q91742 xenopus lae
10	459.5	21.0	818	13	Q9PSV9	Q9psv9 xenopus lae
11	459.5	20.8	822	13	Q91288	Q91288 pleurodeles
12	453.5	20.7	782	11	Q61563	Q61563 mus musculus
13	453.5	20.7	800	11	Q99052	Q99052 mus musculus
14	453.5	20.7	800	11	Q7TS18	Q7ts18 mus musculus
15	447	20.4	796	13	Q91287	Q91287 pleurodeles
16	445.5	20.3	800	11	Q9JHX9	Q9jhx9 rattus norv

Q9ni15 homo sapien  
Q9ni16 homo sapien  
Q42127 xenopus lae  
Q95ml3 bos taurus  
Q800y9 brachydanio  
Q90330 coturnix co  
Q8c3v5 mus musculus  
Q90413 brachydanio  
Q86vi4 homo sapien  
Q8cib8 mus musculus  
Q8tda0 homo sapien  
Q63710 rattus ratt  
Q9ttz3 oryctolagus  
Q60830 mus musculus  
Q60818 mus musculus  
Q800z0 brachydanio  
Q800z1 brachydanio  
Q90200 brachydanio  
Q63827 rattus norv  
Q9gvv7 rattus sp.  
Q63711 rattus ratt  
Q8ixc7 homo sapien  
Q8cfc8 mus musculus  
Q80t10 mus musculus  
Q8cim9 mus musculus  
Q9tt07 canis fami  
Q96ke5 homo sapien  
Q721l9 aplysia cal  
Q8n685 homo sapien

## ALIGNMENTS

## RESULT 1

Q9NSH1 PRELIMINARY; PRT; 422 AA.

ID Q9NSH1  
AC Q9NSH1  
DT 01-OCT-2000 (Tremblrel. 15, Created)  
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)  
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)  
DE Hypothetical protein.  
GN DKFZP761P1010.  
OS Homo sapiens (Human)  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Amysgdala;  
RA Blum H., Bauersachs S., Mewes H.W., Weil B., Wiemann S.;  
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AL353940; CAB89250.1; --  
DR PIR; T48680; T48680.  
DR HSSP; P08631; 1AD5.  
DR GO; GO:0005524; F:ATP binding; IEA.  
DR GO; GO:004713; F:protein-tyrosine kinase activity; IEA.  
DR GO; GO:0016740; F:transferase activity; IEA.  
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.  
DR InterPro; IPR000719; Prot kinase.  
DR InterPro; IPR001245; Tyr\_kinase.  
DR InterPro; IPR008266; Tyr\_kinase\_AS.  
DR Pfam; PF00069; pkinase; 1.  
DR PRINTS; PR00109; TYRKINASE.  
DR PRODOM; PD000001; Prot kinase; 1.  
DR PROSITE; PS00011; PROTEIN KINASE DOM; 1.  
DR PROSITE; PS00109; PROTEIN KINASE\_TYR; 1.  
KW Hypothetical protein; ATP-binding; Kinase; Transferase;  
KW Tyrosine-protein kinase.  
SQ SEQUENCE 422 AA; 47546 MW; B7CD8BC006029D3B CRC64;

Query Match 100.0%; Score 2192; DB 4; Length 422;  
Best Local Similarity 100.0%; Pred. No. 1.9e-186;





```
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003598; IG_c2.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR001245; Tyr_pkinase.
DR InterPro; IPR008266; Tyr_pkinase_AS.
DR Pfam; PF00047; ig; 3.
DR Pfam; PF00069; pkinase; 1.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00408; IGC2; 3.
DR SMART; SM00219; Tyrc; 1.
DR PROSITE; PS00835; IG LIKE; 3.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
KW ATP-binding; Immunoglobulin domain; Kinase; Receptor; Transferase;
KW Tyrosine-protein kinase.
SQ SEQUENCE 828 AA; 93211 MW; 72E2052635D5E323 CRC64;

Query Match 21.3%; Score 467.5; DB 13; Length 828;
Best Local Similarity 30.1%; Pred. No. 1.3e-32;
Matches 122; Conservative 84; Mismatches 162; Indels 37; Gaps 14;

QY 21 EKQYEVIIPTLLVITFL-ILGLVILWLFIREQ--RTQQRSGP--QGIAPVPPRDLWS 75
DB 386 ESRYMIIIT---SGFLAVAMAIVILCRMQTPHKSQTLOTPTVHKLAKFLIRQFSL 442
QY 76 EAGHGNGVALPL-KETSVENFLGATTPAL-----AKQVPREQLSEVL-EQICSGSC 125
DB 443 ESSSSGKSAPLIRITRLSSCAPMLPGVMEVELPLDAKWEFPRDL--VLGKPLGEGCF 500
QY 126 GPIFRA---NMNTGDPSPKPSVILKALKEPAGLHEVQDFLGRIOFQHYLGKHNVLQLEG 182
DB 501 GQVRAEGYGIKDRPEKPVTVAVKMLKONGTDKLSDLSISELMKVIKHNIIINLLG 560
QY 183 CTEKPLPLVMLEDVAGDGLLGLTCCRRDVTMDGLLYDLTE-----KQVYHIGKQ 234
DB 561 VCTQEGFLFVVEYASKGNLREFL-RARRPTPEDA--FDITKVPBELLSFKDLVSCAYQ 617
QY 235 VLLALFLQKHLFHGDVAARNILMOSDLTAKLGLGLAVEYVTRGAISSTQT--IPLKW 292
DB 618 VARGMEYLESKRCIHRDLAARNVLAEDNVMKTDGLFGLARGVHDIDYKTSNGRLPVKW 677
QY 293 LAPERILLRPASTRADVWSFGILLYEMVTILGAPPYPEVPTTSILEHLQRRKIMKRPSST 352
DB 678 MAPEALFDRVYTHQSDIWSFGVLTWEIFTLGGSPYGPVPEELFKLLREGHRMDKPSNCT 737
QY 353 HTMYSIMKSCWRWREADRPSPRELRLRLLEAAIKTADDEAV-LQVP 396
DB 738 HELYMLMRECWHAVPTQRTPFKQLVEHLDRILTAVSEYDLDSMP 782

RESULT 6
ID Q9PSV8 PRELIMINARY; PRT; 829 AA.
AC Q9PSV8;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE GGF receptor 4b.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RA Hongo I., Kengaku M., Okamoto H.;
RT "Differential employment of GGF signaling system for the embryonic
induction."
RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.

DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0016740; P:transferase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003598; IG_c2.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR001245; Tyr_pkinase.
DR InterPro; IPR008266; Tyr_pkinase_AS.
DR Pfam; PF00047; ig; 3.
DR Pfam; PF00069; pkinase; 1.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00408; IGC2; 3.
DR SMART; SM00219; Tyrc; 1.
DR PROSITE; PS00835; IG LIKE; 3.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
KW ATP-binding; Immunoglobulin domain; Kinase; Receptor; Transferase;
KW Tyrosine-protein kinase.
SQ SEQUENCE 829 AA; 93332 MW; 47463466399BF571 CRC64;

Query Match 21.3%; Score 467.5; DB 13; Length 829;
Best Local Similarity 30.1%; Pred. No. 1.3e-32;
Matches 122; Conservative 84; Mismatches 162; Indels 37; Gaps 14;

QY 21 EKQYEVIIPTLLVITFL-ILGLVILWLFIREQ--RTQQRSGP--QGIAPVPPRDLWS 75
DB 387 ESRYMIIIT---SGFLAVAMAIVILCRMQTPHKSQTLOTPTVHKLAKFLIRQFSL 443
QY 76 EAGHGNGVALPL-KETSVENFLGATTPAL-----AKQVPREQLSEVL-EQICSGSC 125
DB 444 ESSSSGKSAPLIRITRLSSCAPMLPGVMEVELPLDAKWEFPRDL--VLGKPLGEGCF 501
QY 126 GPIFRA---NMNTGDPSPKPSVILKALKEPAGLHEVQDFLGRIOFQHYLGKHNVLQLEG 182
DB 502 GQVRAEGYGIKDRPEKPVTVAVKMLKONGTDKLSDLSISELMKVIKHNIIINLLG 561
QY 183 CTEKPLPLVMLEDVAGDGLLGLTCCRRDVTMDGLLYDLTE-----KQVYHIGKQ 234
DB 562 VCTQEGFLFVVEYASKGNLREFL-RARRPTPEDA--FDITKVPBELLSFKDLVSCAYQ 618
QY 235 VLLALFLQKHLFHGDVAARNILMOSDLTAKLGLGLAVEYVTRGAISSTQT--IPLKW 292
DB 619 VARGMEYLESKRCIHRDLAARNVLAEDNVMKTDGLFGLARGVHDIDYKTSNGRLPVKW 678
QY 293 LAPERILLRPASTRADVWSFGILLYEMVTILGAPPYPEVPTTSILEHLQRRKIMKRPSST 352
DB 679 MAPEALFDRVYTHQSDIWSFGVLTWEIFTLGGSPYGPVPEELFKLLREGHRMDKPSNCT 738
QY 353 HTMYSIMKSCWRWREADRPSPRELRLRLLEAAIKTADDEAV-LQVP 396
DB 739 HELYMLMRECWHAVPTQRTPFKQLVEHLDRILTAVSEYDLDSMP 783

RESULT 7
ID Q9I8X3 PRELIMINARY; PRT; 800 AA.
AC Q9I8X3;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Fibroblast growth factor receptor 3.
GN FGFR3.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
```



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OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21184119; PubMed=11287195;
RA Sleptsova-Friedrich I., Li Y., Emelyanov A., Ekker M., Korzh V.,
RA Ge R.;
RT "fgfr3 and regionalization of anterior neural tube in zebrafish.";
RL Mech. Dev. 102:213-217(2001).
DR HSSP; AF157560; AAF80344.1; -.
DR ZFIN; ZDB-GENE-000816-1; fgfr3.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00047; Ig; 3.
DR Pfam; PF00069; pkinase; 1.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00408; Igc2; 3.
DR SMART; SM00219; Tyrc; 1.
DR PROSITE; PS00835; IG LIKE; 3.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
KW ATP-binding; Immunoglobulin domain; Kinase; Receptor; Transferase;
KW Tyrosine-protein kinase.
SQ SEQUENCE 800 AA; 89716 MW; 8092DC0272A5BAD1 CRC64;

Query Match      21.2%; Score 464.5; DB 13; Length 800;
Best Local Similarity 29.2%; Pred. No. 2.3e-32;
Matches 119; Conservative 84; Mismatches 164; Indels 41; Gaps 11;

QY 20 QEQYEVIIIVTLLVTFILLLGVI-----LMLFIREQRTQOORSGP--QGIAPVPPRDL 73
Db 357 REDDYADILIIYVTSVLFILTWIIILCRWMI-----NTQKTLPAFPVQKLSKPLKQV 411
QY 74 SWEAGHGNGVALPL-KETSVENFLGATTPALAKLOVPE-----QLSEVLEQICS 122
Db 412 SLENSNSMNTPLVRIARLSSDGMPLPNVSELESDPKWEFTRTKLTLGKPLGEGCF 471
QY 123 GSCGPIFRANMNTGDPSPKSVILKALKEPAGLHEVQDFLGRIOFHOVLGKHKNLVQLEG 182
Db 472 GOVMAEAGIDKEKPKLTAVAKMLKDDGTDKDLSVSEMEMMKMGKHKNIIINLLG 531
QY 183 CTKEPLVMVLEDAQGDLLGLFWTCRRDVTMTDGLLYD-----LTEXQVYHIG 232
Db 532 ACTQDGLYVLVEYASKGNLREYL-RARRP-----PGMDYSPDTCCKIPNEILTFKDLVSCA 586
QY 233 KQVLLALEFLQEKHLFGDVAARNILMQSDLTAKLGLGLAYEVYTRGAISSTOT--IPL 290
Db 587 YQVARGHEYIASKKCIHRDPAARNVLTEDNVKMIADFGLDARVDHNDIYKKTKTNGSLPV 646
QY 291 KWLAPERLLRPASIRADVMSFGILLYEMVTLGAPPYVEVPTTSILEHLQRRKIMKPPSS 350
Db 647 KWAPEALFDRVYTHQSDVMSYGVLLWEIITLGGSPYGPVPEELFKLLREGHRMDKPN 706
QY 351 CTHWYSIMKSCWRREADRPSRELRLRLAEAIK-TADDEAV-LQVP 396
Db 707 CTHELYMIMRECWAHVPTQRTFQLVEDHDLVLSMTSTDEYLDLSVP 754

RESULT 8
Q91743 ID Q91743 PRELIMINARY; PRT; 828 AA.
AC Q91743;
DT 01-JAN-1998 (T-EMBLrel. 05, Created)
DT 01-JAN-1998 (T-EMBLrel. 05, Last sequence update)
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)

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DE FGF receptor 4 precursor.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96136300; PubMed=8573131;
RA Riou J.F., Clavilier L., Boucaut J.C.;
RT "Early regionalized expression of a novel Xenopus Fibroblast Growth
RT factor receptor in Neuroepithelium.";
RL Biochem. Biophys. Res. Commun. 218:198-204(1996).
DR EMBL; X89807; CAA61930.1; -.
DR FIR; JC4583; JC4583.
DR HSSP; P11362; IFKG.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR001245; Tyr_pkinase.
DR InterPro; IPR008266; Tyr_pkinase_AS.
DR Pfam; PF00047; Ig; 3.
DR Pfam; PF00069; pkinase; 1.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00408; Igc2; 3.
DR SMART; SM00219; Tyrc; 1.
DR PROSITE; PS00835; IG LIKE; 3.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
KW ATP-binding; Immunoglobulin domain; Kinase; Receptor; Signal;
KW Transferase; Tyrosine-protein kinase.
FT SIGNAL 1 38
SQ SEQUENCE 828 AA; 93417 MW; 089EB0D887603524 CRC64;

Query Match      21.0%; Score 461; DB 13; Length 828;
Best Local Similarity 29.4%; Pred. No. 4.9e-32;
Matches 118; Conservative 82; Mismatches 170; Indels 32; Gaps 12;

QY 21 EKQYEVIIIVT--LLVTFILLLGVIILFWLFIREFQRTQOORSGPQGIAPVPPRDLSEAG 78
Db 387 ESRVMDIIIVTSGFLAVAMAIMVILCEMQTPHKSQTLQPTVHKLAKFLDIROFSLESS 446
QY 79 HGNVALPL-KETSVENFLGATTPAL-----AKLQVPREQLSEVL-EQICSGSGPI 128
Db 447 SSGKSSAPLIRITRLSSCAPMLPGVMEVELDLDAKWEFFDRDL--VLGKPLGSGCGV 504
QY 129 FRA---NMNTGDSKPKSVILKALKEPAGLHEVQDFLGRIOFHOVLGKHKNLVQLEGCT 185
Db 505 VRAEGVIEKDRKPKVTVAVKMLKONGTDKDLSDLSISELMKVIKHKNIINLLGCT 564
QY 186 EKPLVMVLEDAQGDLLGLFWTCRRDVTMTDGLLYDTE-----KQVYHIGKQVLL 237
Db 565 QEGFLFVIVEYASKGNLREYL-RARRPPTPEDA--FDITKVPPEELSFKDLVSCAVQVAR 621
QY 238 ALFLEKHLFGDVAARNILMQSDLTAKLGLGLAYEVYTRGAISSTOT--IPLKWLAP 295
Db 622 GMEYLESKRCIHRDLAARNVLAEDNVKMIADFGLDARVDHNDIYKKTSNGLRPVKWAP 681
QY 296 ERLLRPASIRADVMSFGILLYEMVTLGAPPYVEVPTTSILEHLQRRKIMKPPSSCTHTM 355
Db 682 EALFDRVYTHQSDVMSYGVLLWEIITLGGSPYGPVPEELFKLLREGHRMDKPSNCTHEL 741
QY 356 YSIMKSCWRREADRPSRELRLRLAEAIK-TADDEAV-LQVP 396
Db 742 YMLMRECWAHVPTQRTFQLV-HLDRILTAVSEYLDLSMP 782

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Tue Jun 15 09:35:27 2004

RESULT 9  
Q91742 ID Q91742 PRELIMINARY; PRT; 818 AA.  
AC Q91742;  
DT 01-JAN-1998 (TRENBLrel. 05, Created)  
DT 01-JAN-1998 (TRENBLrel. 05, Last sequence update)  
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)  
DE Fibroblast growth factor receptor-4 precursor.  
OS Xenopus laevis (African clawed frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;  
OC Xenopodinae; Xenopus.  
OX NCBI\_TaxID=8355;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=95137391; PubMed=7835703;  
RA Shiozaki C., Tashiro K., Asano-Miyoshi M., Saigo K., Emori Y.,  
RA Shiozaki K.;  
RT "Cloning of cDNA and genomic DNA encoding fibroblast growth factor  
RT receptor-4 of Xenopus laevis."  
RL Gene 152:215-219(1995).  
DR EMBL; D31761; BAA06539.1; -.  
DR PIR; JCA058; JC4058.  
DR HSP; F11362; IFGK.  
DR GO; GO:0005524; F:ATP binding; IEA.  
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.  
DR GO; GO:0004872; F:receptor activity; IEA.  
DR GO; GO:0016740; F:transferase activity; IEA.  
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.  
DR InterPro; IPR007110; IG-like.  
DR InterPro; IPR003598; IG\_c2.  
DR InterPro; IPR007119; Prot\_kinase.  
DR InterPro; IPR001245; Tyr\_pkinase.  
DR InterPro; IPR008266; Tyr\_pkinase\_AS.  
DR Pfam; PF00047; ig; 3.  
DR Pfam; PF00069; pkinase; 1.  
DR PRINTS; PR00109; TYRKINASE.  
DR ProDom; PD000001; Prot\_kinase; 1.  
DR SMART; SM00408; Igc2; 3.  
DR SMART; SM00219; TyrKc; 1.  
DR PROSITE; PS00835; IG\_LIKE; 3.  
DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.  
DR PROSITE; PS00111; PROTEIN\_KINASE\_DOM; 1.  
DR PROSITE; PS00109; PROTEIN\_KINASE\_TYR; 1.  
KW ATP-binding; Immunoglobulin domain; Kinase; Receptor; Signal;  
KW Transferase; Tyrosine-protein kinase.  
FT SIGNAL 1 26 POTENTIAL.  
SQ SEQUENCE 818 AA; 92065 MW; AB741A59E8410E41 CRC64;  
Query Match 21.0%; Score 459.5; DB 13; Length 818;  
Best Local Similarity 29.4%; Pred. No. 6.6e-32;  
Matches 118; Conservative 83; Mismatches 170; Indels 31; Gaps 11;  
QY 21 EKQYEVIIVPT--LLVTIFLLGLVILWLFIREQRTQQQSGPGQGIAPVPPRDLSWEAG 78  
Db 376 ESRMDIIITTSGLAVAMAIVIVLCRMOTPHSKQTLPQPAVHKLAKFLFIQFSLESS 435  
QY 79 HGNVNLPL-KETSVENFLGATTPAL-----AKLQVPREQSEVL-FQICSGSCGPI 128  
Db 436 SSGKSSAPLIRITRLSSCAPMLPGVMEVELPLDAKWEFPRDRL--VLGKPLGEGCGQV 493  
QY 129 FRA---NMWTDGSKPKSVILKALKEPAGLHVQDFLGRIOFHQYLGKHKNLVLEGCCT 185  
Db 494 VRAEGYIEKDRPEKPVTVAVKMLKONGTDKDLISELMELMKVIGKHKNIINLLGVST 553  
QY 186 EKPLYMVLVEDVAGDLGLFWTCRRDVTMDGLLYDLTE-----KQYHIGKQVLL 237

296 ERLILRPASIRADVWSEGLLYEMVTLGAPPYEPVPTTSILEHLQRRKIMRPSCHTMM 355  
671 EALFDVRYTHQSDIWSFGVLTFGLGSGSPYGPVPEELFKLLRGRHMDKPSNCTHEL 730  
356 YSIMKSCWRREARDPSPRELRLRLLEAAIKATADDEAV-LQVP 396  
731 YMLRECWHAVPSQRPFTFKQLVEQLDRILTAVSEYLDLSMP 772  
RESULT 10  
Q9PSV9 ID Q9PSV9 PRELIMINARY; PRT; 818 AA.  
AC Q9PSV9;  
DT 01-MAY-2000 (TRENBLrel. 13, Created)  
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)  
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)  
DE FGF receptor 4a.  
OS Xenopus laevis (African clawed frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;  
OC Xenopodinae; Xenopus.  
OX NCBI\_TaxID=8355;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Hongo I., Kengaku M., Okamoto H.;  
RT "Differential employment of FGF signaling system for the embryonic  
RT induction";  
RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AB007036; BAA22849.1; -.  
DR HSP; F11362; IFGK.  
DR GO; GO:0005524; F:ATP binding; IEA.  
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.  
DR GO; GO:0004872; F:receptor activity; IEA.  
DR GO; GO:0016740; P:transferase activity; IEA.  
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.  
DR InterPro; IPR007110; IG-like.  
DR InterPro; IPR003598; IG\_c2.  
DR InterPro; IPR007119; Prot\_kinase.  
DR InterPro; IPR001245; Tyr\_pkinase.  
DR InterPro; IPR008266; Tyr\_pkinase\_AS.  
DR Pfam; PF00047; ig; 3.  
DR Pfam; PF00069; pkinase; 1.  
DR PRINTS; PR00109; TYRKINASE.  
DR ProDom; PD000001; Prot\_kinase; 1.  
DR SMART; SM00408; Igc2; 3.  
DR SMART; SM00219; TyrKc; 1.  
DR PROSITE; PS00835; IG\_LIKE; 3.  
DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.  
DR PROSITE; PS00111; PROTEIN\_KINASE\_DOM; 1.  
DR PROSITE; PS00109; PROTEIN\_KINASE\_TYR; 1.  
KW ATP-binding; Immunoglobulin domain; Kinase; Receptor; Transferase;  
KW Tyrosine-protein kinase.  
SQ SEQUENCE 818 AA; 92067 MW; A8CBAA341C9230C1 CRC64;  
Query Match 21.0%; Score 459.5; DB 13; Length 818;  
Best Local Similarity 29.4%; Pred. No. 6.6e-32;  
Matches 118; Conservative 83; Mismatches 170; Indels 31; Gaps 11;  
QY 21 EKQYEVIIVPT--LLVTIFLLGLVILWLFIREQRTQQQSGPGQGIAPVPPRDLSWEAG 78  
Db 376 ESRMDIIITTSGLAVAMAIVIVLCRMOTPHSKQTLPQPAVHKLAKFLFIQFSLESS 435  
QY 79 HGNVNLPL-KETSVENFLGATTPAL-----AKLQVPREQSEVL-FQICSGSCGPI 128  
Db 436 SSGKSSAPLIRITRLSSCAPMLPGVMEVELPLDAKWEFPRDRL--VLGKPLGEGCGQV 493  
QY 129 FRA---NMWTDGSKPKSVILKALKEPAGLHVQDFLGRIOFHQYLGKHKNLVLEGCCT 185  
Db 494 VRAEGYIEKDRPEKPVTVAVKMLKONGTDKDLISELMELMKVIGKHKNIINLLGVST 553  
QY 186 EKPLYMVLVEDVAGDLGLFWTCRRDVTMDGLLYDLTE-----KQYHIGKQVLL 237

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Db 554 QGEPFLVIVEYASKGNLREFL-RARRPPTPEDA--FDITKVPDELLSKDLVSCAYQVAR 610
QY 238 ALFFLOEKHLFHGDVAARNILMQSDLTAKLCLGLGLAYEVYTRGAISSTQT--IPLKWLAP 295
Db 611 GMEYLESKRCIHRDLAARNVLVADNVUMKIADFGLAGVHDIIDYKYKTSNGRLPFWKMAP 670
QY 296 ERLLLPASIRADVWFGILLYEMVTGLGAPPYEPVPTSLILEHLQRRKIMKRPSSCTHTM 355
Db 671 EALFDVRYTHQSDIMSGVLTWEIFTLGSGSPYGPVPEELFKLLRGHRMDKPSNCTHEL 730
QY 356 YSIMKSCWRREADRSPRELRLRLLEAAIKTADDEAV-LQVP 396
Db 731 YMLMRECWAHPVSQRPFTFKQLVEQLDRILTAANSEYLDLSMP 772

RESULT 11
Q91288
ID Q91288 PRELIMINARY; PRT; 822 AA.
AC Q91288;
DT 01-NOV-1996 (TremBLrel. 01, Created)
DT 01-NOV-1996 (TremBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TremBLrel. 25, Last annotation update)
DE Fibroblast growth factor receptor.
OS Eukaryotes waltii (Iberian ribbed newt).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Caudata; Salamandroidea; Salamandridae;
OC Pleurodeles.
OX NCBI_TaxID=8319;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93130775; PubMed=1483392;
RA Shi D.L., Feige J.J., Ricu J.F., Desimone D.W., Boucalt J.C.;
RT "Differential expression and regulation of two distinct fibroblast
RT growth factor receptors during early development of the urodele
RT amphibian Pleurodeles waltii";
RL Development 116:261-273(1992).
DR EMBL; X65059; CAA46192.1; -.
DR FIR; B49151; B49151.
DR PIR; S19947; S19947.
DR HSSP; P11362; IFGK.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003598; IG_c2.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR001245; Tyr_kinase.
DR Pfam; PF00047; Ig_3.
DR Pfam; PF00069; pkinase; 1.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00408; IGC2; 3.
DR SMART; SM00219; TyrKc; 1.
DR PROSITE; PS00835; IG LIKE; 3.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS00011; PROTEIN KINASE_DOM; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
KW ATP-binding; Immunoglobulin domain; Kinase; Receptor; Transferase;
SQ Tyrosine-protein kinase.
QY SEQUENCE 822 AA; 92068 MW; 3EC4BA4B9C9AB81A CRC64;

Query Match
Best Local Similarity 20.8%; Score 455.5; DB 13; Length 822;
Matches 118; Conservative 82; Mismatches 169; Indels 35; Gaps 11;

QY 21 EKQYEIVTPT--LLVTFILLLGVILWLFIREQRTQQRSGPOGIAVPVPPDLSEAG 78
Db 383 ETRYTDIIIVTSGSLALLMAAVIVVCLRMQLPPTKTHLEPATVHKLSFFLMROFLESS 442
QY 79 HGGNVALPLKETSVENFLGATTPAL-----AKLQVPRQLSEVL-EQICSGSGC 126

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Db 443 SSGKSTSL--VRVITLSSCTPMLFEGVLEFDLPLDSKWEFFRERL--VLGKPLGSGCFG 498
QY 127 PIFRA---NMNTGDPSPKSVILKALKKEPAGLHEVQDFLGRIOFHQVGLGKHKNLVLEGC 183
Db 499 QVVRAEAYGINKDQDPKAITVAIKIVKDKGTOKELSDLSISELMELKMGKHKNIINLGV 558
QY 184 CTEKIPLYNVLEDVAGDGLLGLFWTCRRDVTMDGLLYDLTE-----KQVYHTGKQV 235
Db 559 CTQDGLYIMIVEYASKGNLREFL-RARRP--PSPDYTFDMTKVPERQLSFQDLVSCSYQV 615
QY 236 LLALFLOEKHLFHGDVAARNILMQSDLTAKLCLGLGLAYEVYTRGAISSTQT--IPLKWL 293
Db 616 ARGMAYLESKRCIHRDLAARNVLVGTENVMKIADFGLAGVHDIIDYKYKTSNGRLPFWK 675
QY 294 APERLLRPASIRADVWFGILLYEMVTGLGAPPYEPVPTSLILEHLQRRKIMKRPSSCTH 353
Db 676 APEALFDVRYTHQSDIMSGVLTWEIFTLGSGSPYGPVPEELFKLLRGHRMDKPSNCTH 735
QY 354 YSIMKSCWRREADRSPRELRLRLLEAAIKTADDEAV-LQVP 396
Db 736 ELYMLMRECWAHPVSQRPFTFKQLVEQLDRILTAANSEYLDLSMP 779

RESULT 12
Q61563
ID Q61563 PRELIMINARY; PRT; 782 AA.
AC Q61563;
DT 01-NOV-1996 (TremBLrel. 01, Created)
DT 01-NOV-1998 (TremBLrel. 08, Last sequence update)
DT 01-OCT-2003 (TremBLrel. 25, Last annotation update)
DE Fibroblast growth factor receptor 3, acid box-deleted isoform.
GN FGFR3 OR FR3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Shimizu A., Seo M.;
RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RX SEQUENCE OF 224-346 FROM N.A.
RX MEDLINE=94209351; PubMed=7512569;
RA Chellatah A.T., McRwen D.G., Werner S., Xu J., Ornitz D.M.;
RT "Fibroblast growth factor receptor (FGFR) 3. Alternative splicing in
RT immunoglobulin-like domain III creates a receptor highly specific for
RT acidic FGF/FGF-1.";
RT J. Biol. Chem. 269:11620-11627(1994).
DR EMBL; AF024638; AAB81604.1; -.
DR EMBL; L26492; AAN21491.2; -.
DR HSSP; P11362; IFGK.
DR MGD; MGI:95524; Fgfr3.
DR GO; GO:0045597; P:positive regulation of cell differentiation; IMP.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003598; IG_c2.
DR InterPro; IPR004074; Ili_receptorI/II.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR001245; Tyr_kinase.
DR InterPro; IPR008266; Tyr_pkinase_AS.
DR Pfam; PF00047; Ig_3.
DR Pfam; PF00069; pkinase; 1.
DR PRINTS; PR01536; INTRLNKIR12F.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00408; IGC2; 3.
DR SMART; SM00219; TyrKc; 1.
DR PROSITE; PS00835; IG LIKE; 3.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS00011; PROTEIN KINASE_DOM; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
KW ATP-binding; Immunoglobulin domain; Kinase; Transferase;
YK Tyrosine-protein kinase.

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SQ SEQUENCE 782 AA; 85871 NW; 90262E44P0CFE49B CRC64;

Query Match 20.7%; Score 453.5; DB 11; Length 782;  
 Best Local Similarity 30.5%; Pred. No. 2.1e-31;  
 Matches 120; Conservative 71; Mismatches 165; Indels 37; Gaps 9;

QY 34 VTIFILLLGVILWLFIREQRTQQRSGPGQIAPV---PPPRDLWSWAGHGNNVALPLKET 90  
 DB 357 VVFFELFILVVAAILCRLRSPPKGLGSPVHKVSRFPLKRVLSLSSNMSNTPL--V 414

QY 91 SVENFLGATTAPALA---KLQVP-----REQLSVEVLQICSGSCGPIFRANMNTGD 137  
 DB 415 RIARLSSGGPGVLANNVSELELPADPKWLSRTRLTGLKPLGEGCFQGVVMAEAGIDKOR 474

QY 138 PSKPKSVILKALKEPAGLHEVQDFLGRIOFHQVLGKHNLVQLEGCTEKLPLYMVLEDV 197  
 DB 475 TAKPVTVAVMKLDKDDATDLSLVSEMEMMKWIGKHNIINLLGACTGGPLYLVEYA 534

QY 198 AQGDLGLFWLTCTRRDVTMTDGLLY-----DLTEKQVYHIGKQVLLALEFLQEKHL 247  
 DB 535 AKGNLREFL--RARRP-----PGMDYSFDACLPBEEQLTKDLVSCAYQVARGMEYLASQK 589

QY 248 FHGDVAARNILMQSDLTAKLGLGLAYEVYTRGAISSTQT--IPLKWLAPERILLRPASI 305  
 DB 590 IHRDLAARNVLVTEDNVMKIADPGLARDVHNLDDYKKTNGRLPVKWMAPALFDRVYTH 649

QY 306 RADVWSFGILLVEMVTLGAPPYEVPTSTLHQLQRKIMKRPSSCTHTMYSIMKSCWRW 365  
 DB 650 QSDVWSFGVLLWEIFLTGSPYGPVVEELFKLLKGHRMDKDPASCTHLYMIMRECWA 709

QY 366 READRPSRELRLRL--AAIKTADDEAVLQVP 396  
 DB 710 VPSQRTFQQLVEDLDRILLVTSTDEYLDLSPV 742

RESULT 13

Q99052 ID Q99052 PRELIMINARY; PRT; 800 AA.

AC Q99052; MEDLINE=91296390; PubMed=1648703;  
 DT 01-JUN-1998 (T-EMBLrel. 06, Created)  
 DT 01-JUN-1998 (T-EMBLrel. 06, Last sequence update)  
 DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)  
 DE Fibroblast growth factor receptor.  
 GN FGFR3 OR FLG-2.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 ON NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Skin;  
 RX MEDLINE=91296390; PubMed=1648703;  
 RA Avivi A., Zimmer Y., Yaron A., Yarden Y., Givol D.;  
 RT "Fig-2, a new member of the family of fibroblast growth factor  
 RT receptors [published erratum appears in Oncogene 1992 Apr;7(4):823].";  
 RL Oncogene 6:1089-1092 (1991).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Skin;  
 RA Avivi A., Zimmer Y., Yaron A., Yarden Y., Givol D.;  
 RT "Errata: lg-2, a new member of the family of fibroblast growth factor  
 RT receptor.";  
 RL Oncogene 7:823-823 (1992).  
 DR ENBL; X58255; GAA41209.1; --  
 DR HSSP; P11362; IFGK.  
 DR MGD; MGI:95524; Fgfr3.  
 DR GO; GO:0045597; P:positive regulation of cell differentiation; IMP.  
 DR InterPro; IPR007110; IG-like.  
 DR InterPro; IPR003598; IG c2.  
 DR InterPro; IPR000719; Prot. kinase.  
 DR InterPro; IPR001245; Tyr. kinase.  
 DR InterPro; IPR008266; Tyr. kinase\_AS.  
 DR Pfam; PF00047; Ig; 3.

DR Pfam; PF00069; pkinase; 1.  
 DR PRINTS; PR00109; TYRKINASE.  
 DR ProDom; PD000001; Prot Kinase; 1.  
 DR SMART; SM00408; IGC2; 3  
 DR SMART; SM00219; TyrKc; 1.  
 DR PROSITE; PS50835; IG LIKE; 3.  
 DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.  
 DR PROSITE; PS00111; PROTEIN KINASE DOM; 1.  
 DR PROSITE; PS00109; PROTEIN KINASE TYR; 1.  
 KW ATP-binding; Immunoglobulin domain; Kinase; Receptor; Signal;  
 KW Transferase; Tyrosine-protein kinase.  
 FT SIGNAL 1 20 POTENTIAL.  
 FT CHAIN 21 800 FIBROBLAST GROWTH FACTOR RECEPTOR.  
 SQ SEQUENCE 800 AA; 87691 NW; B376D47DBE8B312 CRC64;

Query Match 20.7%; Score 453.5; DB 11; Length 800;  
 Best Local Similarity 30.5%; Pred. No. 2.2e-31;  
 Matches 120; Conservative 71; Mismatches 165; Indels 37; Gaps 9;

QY 34 VTIFILLLGVILWLFIREQRTQQRSGPGQIAPV---PPPRDLWSWAGHGNNVALPLKET 90  
 DB 375 VVFFELFILVVAAILCRLRSPPKGLGSPVHKVSRFPLKRVLSLSSNMSNTPL--V 432

QY 91 SVENFLGATTAPALA---KLQVP-----REQLSVEVLQICSGSCGPIFRANMNTGD 137  
 DB 433 RIARLSSGGPGVLANNVSELELPADPKWLSRTRLTGLKPLGEGCFQGVVMAEAGIDKOR 492

QY 138 PSKPKSVILKALKEPAGLHEVQDFLGRIOFHQVLGKHNLVQLEGCTEKLPLYMVLEDV 197  
 DB 493 TAKPVTVAVMKLDKDDATDLSLVSEMEMMKWIGKHNIINLLGACTGGPLYLVEYA 552

QY 198 AQGDLGLFWLTCTRRDVTMTDGLLY-----DLTEKQVYHIGKQVLLALEFLQEKHL 247  
 DB 553 AKGNLREFL--RARRP-----PGMDYSFDACLPBEEQLTKDLVSCAYQVARGMEYLASQK 607

QY 248 FHGDVAARNILMQSDLTAKLGLGLAYEVYTRGAISSTQT--IPLKWLAPERILLRPASI 305  
 DB 608 IHRDLAARNVLVTEDNVMKIADPGLARDVHNLDDYKKTNGRLPVKWMAPALFDRVYTH 667

QY 306 RADVWSFGILLVEMVTLGAPPYEVPTSTLHQLQRKIMKRPSSCTHTMYSIMKSCWRW 365  
 DB 668 QSDVWSFGVLLWEIFLTGSPYGPVVEELFKLLKGHRMDKDPASCTHLYMIMRECWA 727

QY 366 READRPSRELRLRL--AAIKTADDEAVLQVP 396  
 DB 728 VPSQRTFQQLVEDLDRILLVTSTDEYLDLSPV 760

RESULT 14

Q99052 ID Q99052 PRELIMINARY; PRT; 800 AA.

AC Q99052; MEDLINE=91296390; PubMed=1648703;  
 DT 01-OCT-2003 (T-EMBLrel. 25, Created)  
 DT 01-OCT-2003 (T-EMBLrel. 25, Last sequence update)  
 DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)  
 DE Fgfr3 protein.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 ON NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6; TISSUE=Brain;  
 RX MEDLINE=22388257; PubMed=12477932;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.J., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

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RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.
RA Rahey J., Helton E., Kettelman M., Madan A.C., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Maiz M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Brain;
RA Strausberg R.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
RL EMBL; BC053056; AAHS0306.1; -.
SQ SEQUENCE 800 AA; 87676 MW; 2A7215F13F67E5E9 CRC64;

Query Match      20.7%; Score 453.5; DB 11; Length 800;
Best Local Similarity 30.5%; Pred. No. 2.2e-31;
Matches 120; Conservative 71; Mismatches 165; Indels 37; Gaps 9;

QY 34 VTIFLLGLVILWFIREQRTQQRSGPGQIAPV---PPPRDLSEAGHGNNVALPLKET 90
Db 375 VVFFFLVVAAILCLRSPPKGLGSPVHKVSRFPLKRVLSLESSNMSNTPL--V 432
QY 91 SVENFLGATTPALA---KLQVP-----REQLSEVLEQICSGCGPIFRANMNTGD 137
Db 433 RIARISGSGPVLNAVSELELPADPKWELSRLTLTGKPLGEGCFQGVMAEAIGDKDR 492
QY 138 PSKPKSVILKALKEPAGLHEVQDFLGRIQFHQYLGKHNVLQLEGCTEKLPLYMVLVDV 197
Db 493 TAKPTVAVKMLKDDATDKDLSLVSEMEMMKMGKHNIIINLLGACTQGGPLYVLVEYA 552
QY 198 AQGDLGLFWTCRDVMTWMDGLLY-----DLTEKQVYHIGKQVLLAEFLQEKHL 247
Db 553 AKGNLREFL--RARRP----PGMDYSFDACRLPEQLTKDLVSCAYQVARGMEYLASQKC 607
QY 248 FHGDDVAARNILMOSDLTAKLGLGLAYEVYVTRGAISSQT--IPLKWLAPERLLLPA 305
Db 608 IHRDLAARNVLTEDNVMKIADFGARDVHNLDYKKTNGRLPVKMAPEALFDRVYTH 667
QY 306 RADVMSFGILLVEMVTLGAPPYVEVPTTSILEHLQRRKMKRPSCTHTMYSIMKSCWRW 365
Db 668 QSDVMSFGVLLWEIFTLGGSPYGPVPEELFKLLKEGHRMDKPASCTHLYMIMRECWEA 727
QY 366 READRPSRELRLRL--AAIKTADAEAVLQVP 396
Db 728 VPSQRPTFKQVLEDLDRILVTSTDEYLDLSPV 760

RESULT 15
Q91287 PRELIMINARY; PRT; 796 AA.
ID AC Q91287;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Fibroblast growth factor receptor 3.
OS Pleurodeles waltlii (Iberian ribbed newt).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Caudata; Salamandridae;
OC Pleurodeles.
OX NCBI_Taxid=8319;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=94299014; PubMed=8026621;
RA Shi D.L., Launay C., Fromentoux V., Feige J.J., Boucaut J.C.;
RT "Expression of fibroblast growth factor receptor-2 splice variants is
RT developmentally and tissue-specifically regulated in the amphibian
RT embryo.";
RL Dev. Biol. 164:173-182(1994).
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RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=94274759; PubMed=8006062;
RA Shi D.L., Fromentoux V., Launay C., Unbhauser M., Boucaut J.C.;
RT "Isolation and developmental expression of the amphibian homolog of
RT the fibroblast growth factor receptor 3.";
RL J. Cell Sci. 107:417-425(1994).
DR EMBL; X75603; CAAS3271.1; -.
DR FIR; S38579; S38579.
DR HSSP; P11362; IFGK.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0005468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003598; IG_c2.
DR InterPro; IPR000719; Prot kinase.
DR InterPro; IPR001245; Tyr_kinase.
DR InterPro; IPR008266; Tyr_kinase_AS.
DR Pfam; PF00047; ig; 3.
DR Pfam; PF00069; pkinase; 1.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000001; Prot kinase; 1.
DR SMART; SM00408; IGC2; 3.
DR SMART; SM00219; TyrKc; 1.
DR PROSITE; PS00835; IG_LIKE; 3.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS00111; PROTEIN KINASE DOM; 1.
DR PROSITE; PS00109; PROTEIN KINASE TYR; 1.
KW ATP-binding; Immunoglobulin domain; Kinase; Receptor; Transferase;
KW Tyrosine-protein kinase.
SQ SEQUENCE 796 AA; 88288 MW; 226D99A0B6D1D92D CRC64;

Query Match      20.4%; Score 447; DB 13; Length 796;
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QY 92 VENFLGATTPALAKLQVP-----REQLSEVLEQICSGCGPIFRANMNTGDPSPK 141
Db 428 LSSDGPMLNAVSELELPADPKWELSRSLTLTKPLGEGCFQGVWADAVGTEKDPNKA 487
QY 142 KSVILKALKEPAGLHEVQDFLGRIQFHQYLGKHNVLQLEGCTEKLPLYMVLVDVAQGD 201
Db 488 TSVAVKMLKDDATDKDLSLVSEMEMMKMGKHNIIINLLGACTQGGPLYVLVEYASKGN 547
QY 202 LLGFLWTCRDVMTWMDGLLY-----DLTEKQVYHIGKQVLLAEFLQEKHLFHGD 251
Db 548 LREYL--RARRP----PGMDYSFDTCKLPEEQTLTKDLVSCAYQVARGMEYLASQKCIHRD 602
QY 252 VAARNILMOSDLTAKLGLGLAYEVYVTRGAISSQT--IPLKWLAPERLLLPASTRADV 309
Db 603 LAARNVVTDDNNVKIADFGARDVHNLDYKKTNGRLPVKMAPEALFDRVYTHQSDV 662
QY 310 WSFGILLVEMVTLGAPPYVEVPTTSILEHLQRRKMKRPSCTHTMYSIMKSCWRWREAD 369
Db 663 WSFGVLLWEIFTLGGSPYGPVPEELFKLLKEGHRMDKPANCTHLYMIMRECWAHPVPSQ 722
QY 370 RSPRELRLRL--AAIKTADAEAV-LQVP 396
Db 723 RPTFKQLVEDLDRILVTSTDEYLDLSPV 751

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